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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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TCNVAHPASSTKVDKK EEPRVEITQNPCPPLKECPPCAAPDLLGGFSVFIFPPRIKDV
LMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPI
QHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLPPPAEEMTKREFSLT
                                                                                                                                                                                                                                                                                                /tissue_type="pancreas"
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was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3'
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                                                                                                                                                             /db_xref="FANTOM_DB:1810060009"
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                                                                                                                                                                                     /db_xref="MGD:MGI:1910399"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB25349.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="MGD:MGI:96443"
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                                                             Location/Qualifiers
                                                                                                                                                                                                                                              /clone="1810060009"
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                                                                                                                                     /strain="C57BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Igh-1"
56. .1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Igh-1"
                                        SOLR
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                                                                                                                                                                                                                                                                        /sex="male"
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                                        end: SstI. Host:
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COOZ OC: 04:01 T

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/lab_host="DH10B"

/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This close is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E1.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn source libraries are closed unidirectionally with Oligo(dT source libraries are closed unidirectionally with Oligo(dT) Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Kargil, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3103 row: H column: 12 EST 26-JAN-2001 Proc. Natl. Acad. Sqi. U S. A. 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased gene expression patterns during pre-implantation mouse devalopment, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1367-1378. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. ö 771 ACAATCAACCCTGTCCTCCATGCAAGAGTGTCACAAATGCCCAGCTCCTAACCTCGAG 830 H3103H12-3 NIA Mouse 15K CDNA Clone Set Mus musculus CDNA clone H3103H12 3', mRNA sequence. /clone_lib="NIA Mouse 15K cDNA clone Set"
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/dev_stage="Clones arrayed from a variety of cDNA 711 GCTCACCCAGCAGCACCACGT¢GACAAAAACTTGAGCCCAGCGGGCCCATTTCA 0; Gaps National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA 52.3%; Score #30.8; DB 12; Length #42; 99.2%; Pred. No. 4.4e-162; Live 0; Mismatches 7; Indels 0; /db_xref="niaEST:H3103H12-3" Email: cdna@lgsun.grc.nia.nih.gov /organism="Mus musculus" Plate: H3103 row: H column: 12 Seq primer: -21M13 Forward High quality sequence stop: 842 /db_xref="taxon:10090" Location/Qualifiers /strain="C57BL/6J" /clone="H3103H12" Contact: George J. Kargul BG071858.1 GI:12554427 Unpublished (2001) Other_ESTs: H3103H12-5 Laboratory of Genetics (bases 1 to 842) libraries" Conservative .842 Mus musculus house mouse. Similarity POLYA=Yes 835; Query Match Source BG071858/c DEFINITION ORGANISM ACCESSION BASE COUNT REFERENCE AUTHORS KEYWORDS Matches FEATURES TITLE Dp á

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1431 TACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCT 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1311 CCAGTCCTGGACTCTTGACGGTTCTTACTTATATAGCAAGCTCAATATGAAAACAAGC 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1371 AAGTGGGAGAAACAGATTCCTTCTCATGCAACGTGAGACACGGGGTCTĠAAAAATTAC 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1491 CAGGICCIAAGAGACACIGGCACCCATAICCAIGCAICCCIIGIAIAAAIAAAGCAICCA 1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1131 ATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCA 1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1251 GACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCGCA 1310
                                                                                                                                                                                                                                                                                                                        951 AGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGAT 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                             1011 TACAACAGTACTATCCGGGTGGTCAGCACCTCCCCATCCAGCACCAGGACTGGATGAGT 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1071 GGCAAGGAGTTCAAATGCAAGGTCAACAAAAAGACCTCCCATCACCCATCGAGAGAACC 1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 AAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAAATTAC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 CCAGTCCTGGACTCTGACGGTTCTTACTTCATATACAGCAAGCTCGATATAAAAACAAGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 GAGCAGTIGICCAGGAAAGAIGICAGICICACTIGCCIGGICGIGGGCITCAACCCIGGA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   662 ACACCCAAGGTCACGTGTGTGTGGTGGTGTGAGCGAGGATGACCCAGACGTCCGGATC 603
                                                                                                                                                                                                                                                                                                                                                                                   602 AGCTGGTTTGTGAACAACGTGGAAGTACACACACGTCAGACACAAACCCATAGAGAGGAT 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       542 TACAACAGTACTATCCGGGTGGTCAGTGCCCTCCTCATCCAGGACCAGGACTGGATGAGT 483
                                                                                  GGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTG 890
                                                                                                                                         722 GGIGGACCAICCGICTICAICTICCCICCAAAIAICAAGGAIGIACICAIGAICTCCCIG 663
                                                                                                                                                                                                    891 ACACCCAAGGTCACGTGTGGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 TACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCCCCCACAAAGCTCT 63
                     782 ACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAG 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1551 GC 1552
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1247 TGGAGACATCAGTGT-GGAGTGGACCAGCGATACAGAGGAGAGAGTACAAGGACA 1305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1187 AGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACC 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             949 TCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACACAAACCCATAGAGAGG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1009 ATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAG-CACCAGGACTGGATG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1068 AGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCCATCACCCATGGAGAGA 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 ATTACAACAGTACTATCCGGGTGGTCAGTGCCCTCCCCATCCAGACACCAGGACTGGATG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGGGGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    889 TGACACCCAAGGTCACGTGTGTGGTGGTGTGAGGGAGGATGACCCAGACGTCCAGA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            649 TGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCG 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  709 TTGCTCACCCAGCCACCACCACGCTGGACAAAAACTTGAGCCCAGCGGGCCCATT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               769 CAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCG 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCCAGCTCCTAACCTCG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               829 AGGGIGGACCAICCGICIICAICIICCCICCAAAIAICAAGGAIGIACICAIGAICICCC 888
                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 288 c 226 g 188 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Lu29"
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Stem cell origin."
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8748 row: o column: 04
High quality sequence stop: 735.
Location/Qualifiers
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40.1%; Score 636.6; DB 10; Length 977;
Best Local Similarity 95.9%; Pred. No. 7.3e-122;
Matches 707; Conservative 0; Mismatches 24; Indels 6;
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                                                                                                                                                                                                                                                                                            /strain="CZECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
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EST 21-JUL-2000

linear

mRNA

977 bp

601217516F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586779 5'

BE367725.1 GI:9313153

house mouse. Mus musculus

ORGANISM

mRNA sequence. BE367725

BE367725

SFINITION

3367725

CESSION

EYWORDS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

NIH-MGC http://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)

(bases 1 to 977)

EFERENCE AUTHORS Contact: Robert Strausberg, Ph.D.

Unpublished (1999)

JOURNAL

OMMENT

Db 181 CICCIGCAGTCIGGACTCIACACIAIGAGCAGCICAGIGACIGICCCCICCAGCACCIGG	684	241	VY /44 AAACTTGAGGGGCCCATTTGAACCCCTGTCCTCCATGCAGGAGTGT 	QY 804 CACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAT	QY 864 ATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGGTGGTGGATGTG	Qy 924 AGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAC	QY 984 GCTCAGACACAAACCCATAGAGAGTTACAACAGTACTATCCGGGTGGTCAGCACCTC	Qy 1044 CCCATCCAGCACCAGGACTGGATGGCAAGGAGTTCAAATGCAAGGTCAACAAAA	Qy 1164 CAAGTATACATCTTGCCGCCACCAGGAGGAGCAGTTGTCCAGGAAA 1208 	RESULT 5 BF135247 LOCUS DEFINITION 601781917F1 NCI_CGAP_LU30 MUS musculus cDNA clone IMAGE:4009636 5', ACCESSION BF135247 VERSION BF135247.1 GI:10974287 KEYWORDS EST.	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertek Mammalia; Eutheria; Rodentia; Sciurognathi; Mu 1 (bases 1 to 754) NIH-MGC http://mgc.nci.nih.gov/	International institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: Gapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc.	UNA Sequencing by:Incyte Genomics, Inc. Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov b column: 05 High quality sequence stop: 614.
TGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATCCAGAGGAGAACTACAGTGACA 660	CCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATAGGAAGCTCAATATGAAAA 1365 	CAAGCAAGTGGGAGAAA 1382		FSE 24 - OCT	601783787F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4011837 5', mRNA sequence. BF136899.1 GI:10975939		Mammalia; Eutheria; Rodentia; Cranlada; Verrebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 819) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov	found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM9251 row: m column: 22 High quality sequence stop: 716. Location/Oualifiers:	ulus" 90" 37" P_Lu30" metastatic to mammary"	/nocem-Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 206 a 234 c 205 g 173 t 1 others	tch al Similarity 93.2%; Score 628.8; DB 12; Length 819; 713; Conservative 0; Mismatches 43; Indels 9; Gaps 5; 445 TCACCGTCTCCTCAGCCAAAACAACAACCATCAGTCTATCCACTGGCCCTGGGTGG 504	1 TCACAGTCTCCTCAGCCAGAACAACACCCCCATCAGTCTATCCACTGGCCCTGGGTGTG 60 505 GAGATACAACTGGTTCCTC - CGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAG 563

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1117 CCATCGAGAG-AACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATC 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1060 ACTGGATGAGTGGCAA-GGAGTTCAAATGCAAGGTCAAC-AACAAAGACCTCCCATC-AC 1116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      940 ACGICCAGAITAGCIGGITIGIGAACAACGIGGAAGTACACACACACACACACAAAACCC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 ACGTCCAGATCAGCTGG-TTGTGAACAACGTGGAAGTACACACACCACAGACACAAA-CC 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545 ATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAG-TGCCTCCCCATCCAGCAACAGG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  580 GGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAGTCTGGAC 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  820 CTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             880 IGAICICCCIGACACCCAAGGICACGIGIGGIGGIGGAIGIGAGCGAGGAIGACCCAG 939
                                                                                                                                                                                                                                                                                                                                           460 CCAAAACAACCCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTT 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 TCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCA 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 CCIGCAGCGIIGCICACCCAGCCAGCACCACGCIGGACAAAAAACTIGAGCCCAGCG 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 GGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                            520 CCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTT 579
                                                                                                                                                                                                                                                                                                                                                                      7; Gaps
                                                                                                                                               Investigator providing samples: Gilbert Smíth, NIH"
230 c 174 g 150 t
                                                                                                                                                                                                                                                39.2%; Score 621.8; DB 12; Length 754; 95.5%; Pred. No. 8.9e-119;
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                 0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1176 TTGCCGCCACCAGCAGAGCAGTTGTCCAG 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     724 TIGGCGCCACCAGCAGACGIGTCCCGG 752
                                                                                                                                                                                                                                                                                                      Matches 715; Conservative
                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                  SE COUNT
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BE134114 cares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:1531775 3' similar to gb:X67210 M.musculus rearranged immunoglobulin gamma 2b heavy (MOUSE);, mRNA sequence.

E134114/C OCUS EFINITION

ESULT 6

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1368 AGCAAGTGGGAAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAAT 1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1008 GATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1248 GGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACC 1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1308 GCACCAGTCCTGGACTCTGACGGTTCTTACTTATATAGCAAGCTCAATATGAAAACA 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               948 AICAGCIGGIIIGIGAACAACGIGGAAGIACACACACAGCICAGACACAAACCCAIAGAGAG 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1068 AGTGGCAAGGAGTTCAAATGCAAGGTCAACAAAAAGACCTCCCATCACCATCGAGAGA 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1128 ACCAICTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCA 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote—"Vector: pr773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was prepared to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library is normalized. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 GCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATACAGCAAGCTCGATATAAAAACA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 AGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGGGGGTTGAAAAT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            572 GATTCACCAGGTACTATCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATG 513
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified pT/T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.1%; Score 604.8; DB 10; Length 647; 97.3%; Pred. No. 3e-115; tive 0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="texon:10090"
/clone="IRAGE:153175"
/clone_lib="Soares_mammary_gland_NMLMG"
                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 440.
Location/Qualifiers
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                 BE134114.1 GI:8596614
                                                                                                                                                 (bases 1 to 647)
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                                                                                                                                                                                                                Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                .647
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                                                                                     Mus musculus
                                                                house mouse.
                                                                                                                                                                                                                                                                                                                                                 MGI:947875
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BE134114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 615;
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                                                                                  ORGANISM
ACCESSION
                                                                                                                                                                            AUTHORS
                                                                                                                                                   REFERENCE
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                                          KEYWORDS
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COOK OF . OF .

		qa	570 GAGGATTACACCA
	1428 TACTACCTGAAGAAGACCATCTCCCGGTCTCCCGGGTAAATGAGCTCAGCACCCACAAAGC 1487	·	CONTRACTOR SOL
	152 TACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAGC 93	7	003 AIGAGIGGCAAGG
Qy 1488	38 TCTCAGGTCCTAAGAGACACTGGCACCCATATCCATGCATCCCTTGTATAAATAA	gn	510 AGAGTTGGCAAGG
qq	92 TITCAGGICCTAAGAGACACIGGCACCCAIATCCAIGCAICCCIIGIAIAAAAAAGAI 33	Qy 1	1125 AGAACCATCTCAA
Qy 1548	8 CCAGCAAAGCCTGGTACCATGTAAAAAAAA 1579	qq	450 AGAACCATCTCAA
ପ୍ର		Oy 1	1185 CCAGCAGAGCAGT
RESULT 7			390 CCAGCAGAGCAGT
BF148722/c	2007	Qy 1	1245 CCTGGAGACATCA
DEFINITION	bride 122	qq	330 CCTGGAGACATCA
	simitar to SW:GCB_MOUSE P01866 IG GAMMA-2B CHAIN C REGION. ;, mRNA sequence.	Qy 1	1305 ACCGCACCAGICC
ACCESSION VERSION	BF148722 BF148722.1 GI:11030117	qa	270 ACCGCACCAGTCC
SOURCE	EST. house mouse.	Qy 1.	1365 ACAAGCAAGTGGG
ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata: Enteleostomi:	qq	210 ACAAGCAAGTGGG
REFERENCE	Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	0y 1	1425 AATTACTACCTGA
AUTHORS TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute. Cancer General Anatom.	qa	150 AATTACTACCTGA
TANGIJOE	Tunor General Control Cancer Genome Anaromy Froject (CGAP),	0y 1	1485 AGCTCTCAGGTCC
	Other ESTS: uv34a01.yl		90 AGCTCTCAGGTCC
	Contact: Kobert Strausberg, Ph.D. Email: cqapbs-r@mail.nih.gov		
	Tissue Procurement: Gilbert Smith, Ph.D.		1545 CATCCAGCAAAGC
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DÞ	30 CATCCAGCAAAGCC
	DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be	RESULT 8	
	Iound through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov/image/html/iresources.shtml	AA882246 LOCHS	37882246
	MGI:1422184	DEFINITION	vx42e07.rl Strat
	Seq primer: -40Up from Gibco High quality sequence stop: 423.		IMAGE:1277892 5' (HUMAN); gb:X672 heavy (Monse).
Source	Location/Qualifiers	ACCESSION	AA882246
	/organism="Mus musculus" /strain="C2ECH II"	KEYWORDS	EST.
	/db_xref="taxon:10090"	SOURCE ORGANISM	house mouse. Mus musculus
	/clone_lib="locater" /clone_lib=" /clone_lib="locater" /clone_lib=" /clone_		Eukaryota; Metaz Mammalia; Euther
	/lab_host="Lumor, metastatic to mammary" /lab_host="DH10B"	REFERENCE	1 (bases 1 to 7
	/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; transgenic model WNT-1, expression driven by	CACH	Geisel, S., Kucab
	MMTV-LTR enhancer; Cloned unidirectionally, Primer: Oligo dT. Library constructed by Life Technologies		Theising, B., Wyl
ASE COUNT	Investigator providing samples: Gilbert Smith, NIH" 122 a 140 c 171 g 205 t 1 others	TITLE	waterston, R. The WashU-HHMI M
RIGIN		COMMENT	Contact: Marra M
Query Matc Best Local	Query Match 37.1%; Score 589; DB 12; Length 639; Best Local Similarity 95.9%; Pred. No. 5.7e-112:		WashU-HHMI Mouse Washington Unive
Matches 60	604; Conservative 0; Mismatches 26; Indels 0; Gaps 0;		Tel: 314 286 180
y 94.	945 CAGATCAGCTTGTGAACAACGTGGAAGTACACACACACAC		Email: mouseest@
р 63.	O CAGATCAAGTTGGTTGATAACAACGTGGAAGTACACCAAGTTCACACAAACCCATAGA 571		This clone is av IMAGE Consortium

1005 GAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGG 1064

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TTGTCCAGGAAAGÀTGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAAC 1244
                                                                                                                                                                                                                                                                                                                                                                                                      CTGGACTCTGACG¢TTCTTACTTCATATATAGCAAGCTCAATATGAAA 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAAAACAGATT¢CTTCTCATGCAACGTGAGACACGAGGGTCTGAAA 1424
                                           GAGTTCAAATGCAAGGTCAACAACAAGACCTCCCATEACCCATCGAG 1124
                                                                                                                                AAAATTAAAGGGC#AGTCAGAGCTCCACAAGTATACATCTTGCCGCCA 1184
                                                                                                                                                                                                                                                                                                               AGTGTGGAGTGGAÇCAGCAATGGGCATACAGAGGAGGAACTACAAGGAC 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAAGACCATCT¢CCGGTCTCCGGGTAAATGAGCTCAGCACCCCACAA 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 26-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
aba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
ylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                CTGGACTCTGACGGTTCTTACTTCATATACAGCAGCTCGATATAAAA 211
AGTACTATCCGGGIGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            azoa; Chordata; Craniata; Vertebrata; Euteleostomi;
eria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           703 bp mRNA linear EST 26-MAR-19 atagene mouse lung 937302 Mus musculus cDNA clone 5' similar to gb:S65761 IG GAMMA-2 CHAIN C REGION 7210 M.musculus rearranged immunoglobulin gamma 2b mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the MANCE Consortium (info@image|llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                             k Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           se EST Project
Fersity School of MedicineP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          @watson.wust1 edu
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source
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                                                                                    DEFINITION
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                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                REFERENCE
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                               RESULT 9
BG084699
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                                                                                                                                                                  KEYWORDS
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                                                                                                                                                VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1120 TCGAGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGC 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1180 CGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCT 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .240 TCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAA-TGGGCATACAGAGGAGAACTAC 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1299 AAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGCAAGCTCAAT 1358
                                                                                                                                                                                                       1000 ATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGG 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1060 ACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCATCACCA 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          540 AA-GACACCGCACCAGTCTGGACTCTGACGGTTCTTACTTCATATGCAGCAAGCTCGGT 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      599 AATAAAAACAAGCGAGTGGGAGAAAACAGATTCCTTCTCCTGCACCCTTGGACACCGGGG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420 CGCCAGCAGCAGCAGTTGTCAAGGAAAGAAGTCAGTCTCACTTGCCTGGTCGGTGGGC 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    760 GGCCCATTTCAACAATCAACCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTC 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       820 CINACCICGAGGGIGGACCAICCGICITCAICTICCCICCAAAIAICAAGGAIGIACICA 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               940 ACGICCAGAICAGCIGGITIGIGAACAACGIGGAAGIACACACAGCICAGACACAAACCC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 | GCCGATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 35.3%; Score 560.4; DB 9; Length 703; bl Similarity 91.8%; Pred. No. 4.7e-106; 647; Conservative 0; Mismatches 52; Indels 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1416 GGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCG 1460
                                                                                                                                                    /clone_lib="Stratagene mouse lung 937302'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: -28m13 rev1 ET from Amersham
                                                                        /organism="Mus musculus"
                     High quality sequence stop: 271.
                                                                                             /strain="C57BL/6 x CBA"
                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:1277892"
                                     Location/Qualifiers
                                                                                                                                                                                       /tissue_type="lung"
                                                                                                                                                                          /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                     SE COUNT
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/note="Vector: pSPORT1; Site_1: Sall; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNa libraries (including preimplantation stage embryo from unfertilized egg to blastocyst, embryos part of E7.5 embryos extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone set has been freely distributed to the community. Please visit http://lgun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3103 row: H column: 12 Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     )-Not primers. References include: (1) Genome-wide expression profilling of mid-gestation placenta and embryousing a 15,000 mouse developmental CDNA microarray, 2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse develolpment, 2000,
Development, 127: 1737-1749; (3) Genome-wide mapping of
                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 571)
Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.
7.S., Carter,M.G. and Ko,M.S.H.
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                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                         H3103H12-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIA Mouse 15K cDNA Clone Set" /sex="Clones arrayed from a variety of cDNA libraries" /dev_stage="Clones arrayed from a variety of cDNA
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0; Mismatches 2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National 102124-6820, USA
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdne@lgsun.grc.nia.nih.gov
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   linear
         mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="niaEST:H3103H12-5"
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176 c 136 g 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                   H3103H12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="H3103H12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: George J. Kargul
                                                                                                                                   BG084699.1 GI:12567263
                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
Other_ESTs: H3103H12-3
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                                                                                                                                                                                                         house mouse.
         BG084699
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The part

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TICCTCCGTGACTCTGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGAC 577
                578 TIGGAACTCTGGATCCCTGTCCAGCAGTGTGCACCTTCCCAGCTCTCCTGCAGTCTGG 637
                                                                       538 ACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGT 697
                                                                                                                               698 CACCTGCAGCGTTGCTCACCCAGCAGCACCACGGTGGACAAAAAACTTGAGCCCAG 757
                                                                                                                                                                                       758 CGGCCCATTICAACAATCAACCCCTGTCCTGCAAGGAGTGTCACAAATGCCCAGC 817
                                                                                                                                                                                                                                             818 TCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACT 877
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EST 01-FEB-2002
                            BM243266 552 bp mRNA linear EST 01-FEB-200 K0644A12-3 NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+) CDNA Library (Long) Mus musculus CDNA clone K0644A12 3', mRNA
                                                                                                                             sednence
                                                           EFINITION
M243266/c
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BM243266.1 GI:17878536 CCESSION EYWORDS

ERSION

house mouse.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus ORGANISM EFERENCE

1 (bases 1 to 552)
Plao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H. Systematic Analyses of NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+) cDNA Library (Long) Unpublished (2001)

JOURNAL

Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: K0644 row: A column: 12
Seq primer: -21M13 Forward Seq primer: -21M13 Forward High quality sequence stop: 552 Contact: Dawood B. Dudekula

/organism="Mus musculus" /strain="C57BL/6NCr" Location/Qualifiers POLYA=Yes

source

SATURES

/db_xref="niaEST:K0644A12-3" /db_xref="taxon:10090"

/clone="K0644A12" /clone_lib="NIA Mouse Hematopoietic Stem Cell

Not: Mouse color project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 1: 1553-1558 (2001). [PMID: 11544199]). Total RNAS were obtained from Drs. Dennis Taub, Dan Longo (National Institute on Aging, USA), Jonathan Keller (National Cancer Institute, USA). Double-stranded cDNAs were synthesized (Lin-/c-Kit-/Sca-1+) cDNA Library (Long)" /tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+ /note="Vector: pSPQRT1 (Invitrogen); Site_1: Sal1; Site_2 mixture by the standard chemical method. The average insert size is about 2.2 kb. The library was constructed by Yulan Piao (NIA)." The DH10B E. coli host was transformed with the ligation /dev_stage="Age approx.10 weeks old" /lab_host="DH10B" 150 g 125 c

0; Gaps cch 34.3%; Score 544; DB 13; Length 552; al Similarity 99.1%; Pred. No. 1.2e-102; 547; Conservative 0; Mismatches 5; Indels Local Similarity Query Match Matches

170 t

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BASE COUNT

ORIGIN

ö 1018 GTACTATCCGGGTGGTCAGCACCCTC¢CCATCCAGCACCAGGACTGGATGAGTGGCAAGG 1077 1138 AAATTAAAGGGCTAGTCAGAGCTCCA¢AAGTATACATCTTGCCGCCACCAGCAGCAGT 1197 1078 AGTTCAAATGCAAGGTCAACAACAAA¢ACCTCCCATCACCCATCGAGAGAACCATCTCAA 1137

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1198 TGTCCAGGAAAGATGTCAGTCTCACT#GCCTGGTCGTGGGCTTCAACCCTGGAGACATCA 1257 g g

1258 GTGTGGAGTGGACCAGCAATGGGCATACAGAGAGACTACAAGGACACGCACCAGTCC 1317

1318 IGGACICIGACGGIICITACIICATAȚATAGCAAGCICAATAIGAAAACAAGCAAGIGGG 1377

1378 AGAAAACAGATTCCTTCTCATGCAACGTGAGGGTCTGAAAAATTACTACCTGA 1437

1438 AGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCACAAAGCTCTCAGGTCC 1497

1498 TAAGAGACACTGGCACCCATATCCAT¢CATCCCTTGTATAAATAAAGCATCCAGCAAAGC 1557

1558 CTGGTACCATGT 1569

FINITION

CESSION

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ORGANISM

FERENCE AUTHORS JOURNAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Resobtained from Drs. Dennis Taub, Dan Longo (National Institute on Aging, UGA), Jonathan Keller (National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
                                                                                                                                                              linear EST 01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 552)
Plao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Luo,A., Carter,M.G., Taub,D., Longo,D.L., Keller,J. and Ko,M.S.H.
Systematic Analyses of NIA Mouse Hematopoletic Stem Cell
(Lin-/C-Kit-/Sca-1+) cDNA Library (Long)
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                  K0647B06-3 NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1+)
cDNA Library (Long) Mus musculus CDNA clone K0647B06 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory of Genetics
National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: KOGA7 row: B column: 06
Seq primer: -21M13 Forward
High quality sequence stop: 552
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(Lin-/c-Kit-/Sca-1+) cDNA Library (Long)"
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/lab_host="DH10B"
                                                                                                                                                                 mRNA
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/db_xref="taxon:10090"
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                               12 CTGGTACCATGT 1
Mus musculus
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ATURES

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uw24c07.x1 Soares_thymus_2NbMT Mus musculus cDNA clone
IMAGE:3417612 3' similar to SW:GCB_MOUSE P01866 IG GAMMA-2B CHAIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 26-SEP-2000
                                                     1018 GTACTATCCGGGTGGTCACCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGG 1077
                                                                                                                              1078 AGTICAAAIGCAAGGICAACAACAAGACCICCCAICACCAICGAGAGAACCAICICAA 1137
                                                                                                                                                                                                       1138 AAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGT 1197
                                                                                                                                                                                                                                                                                 1198 TGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCA 1257
                                                                                                                                                                                                                                                                                                                                                          1258 GIGIGGAGIGGACCAGCAAIGGGCATACAGAGGAGAACTACAAGGACACCGCACCAGICC 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1438 AGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCCACAAAGCTCTCAGGTCC 1497
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 AGAAGACCATCTCCCGGTCTCCCGGGTAAATGAGCTCAGGCACCCACAAAGCTCTCAGGTCC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMAGE Consortium (info@image.linl.gov) for further information.
                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                   5; Indels
   Pred. No. 1.2e-102;
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99.1%; Preu. ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE:3417612 3' similar 1
REGION. ; mRNA sequence.
BE852279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE852279.1 GI:10310618
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Unpublished (1997)
                      Matches 547; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 CTGGTACCATGT 1
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/strain="C57BL/6J"

Query Match

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3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                          1023 ATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTC 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .083 AAATGCAAGGTCAACAACAAGACCTCCCATCCAGCGAGGAACCATCTCAAAAAT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.8%; Score 536; DB 12; Length 547; 99.1%; Pred. No. 5.6e-101; 1ve 0; Mismatches 5; Indels 0
                                             /clone_lib="Soares_thymus_2NbMT"
/db_xref="taxon:10090"
/clone="IMAGE:3417612"
                                                                                         /tissue_type="Thymus"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                       149 g
                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 539; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       103
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Query Match

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BASE COUNT

Query Match source BASE COUNT δ g q δ ŏ g g à ŏ 1203 AGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTG 1262 1143 AAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGCAGTTGTCC 1202 1263 GAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGGAC 1322 1383 ACAGATTCCTTCTCATGCAACGTGAGACACGGGGTCTGAAAATTACTACCTGAAGAAG 1442 443 ACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGA 1502 187 ACAGATICCTICTCATGCAACGIGAGACACGAGGGTCTGAAAAATTACTACCTGAAGAAG 128 1563 ACCA 1566 7 ACCA 4

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EST 24-OCT-2000

linear

mRNA

530 bp

601779503F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4007424 5'

BF134589.1 GI:10973629

mRNA sequence. BF134589

BF134589

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F134589

CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencity by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. 984 GCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTC 1043 1044 CCCATCCAGCACCAGGACTGGATGAG‡GGCAAGGAGTTCAAATGCAAGGTCAACAAA 1103 1104 GACCTCCCATCACCCATCGAGGAAC¢ATCTCAAAATTAAAGGGCTAGTCAGAGCTCCA 1163 1164 CAAGTATACATCTTGCCGCCACCAGCAGAGAGTTGTCCAGGAAAGATGTCAGTCTCACT 1223 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 530) 744 AAACTTGAGCCCAGGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGT 803 804 CACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAT 863 864 ATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGGTGGTGGTGGTGTG 923 241 GCTCAGACACAAAACCCATAGAGAGTACAACAGTACTATCCGGGTGGTCAGTCCCTC 300 924 AGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACA 983 301 CCCATCCAGCACCAGGACTGGATGAGTGGAGGAGTTCAAATGCAAGGTCAACAAAA 360 1 AAACTTGAGCCCAGCGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGT 60 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NIH-MGC http://mgc.nci.nih.ģov/. National Institutes of Health, Mammalian Gene Collection (MGC) 0; Gaps Investigator providing samples: Gilbert Smith, NIH" 150 c 126 g 105 t 1224 TGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAG 1273 DB 12; Length 530; /clone="IMAGE:4007424" /clone_lib="NCI_CGAP_bu30" /tissue_type="tumor, metastatic to mammary" /lab_host="DH108" 2; Indels Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. 33.2%; Score 526.8; DB 1: 99.6%; Pred. No. 4.5e-99; Live 0; Mismatches 2 Plate: LLAM0240 row: f column: 01 High quality sequence stop: 528. Location/Qualifiers Ph.D. /organism="Mus musdulus" /db_xref="taxon:10090" Contact: Robert Strausberg, /strain="CZECH II" Unpublished (1999) Matches 528; Conservative Mus musculus Best Local Similarity 149 a ORGANISM TITLE JOURNAL AUTHORS REFERENCE FEATURES COMMENT SOURCE g δ g Q

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Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                         1264 AGTGGACCAGCAATGGCCATACAGAGGAGAACTA-CAAGGACACCGCACCAGTCCTGGAC 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1441 AGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCCACAAAGCTCTCAGGTCCTAA 1500
                                                                                                                                                                                                                                                                                           1204 GGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGG 1263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1084 AATGCAAGGTCAACAACAAGACCTCCCATCACCCATCGAGAACCATCTCAAAAATTA 1143
                                                                                                                                                                                      1144 AAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCA 1203
                                                                                                                                                                                                                                                                                                                   242 GGAAAGATGTCAGTCTCACTTGTCTGGTCGGCTTCAACCCTGGAGACATCAGTGTGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 AGACCATCTCCCGGTCTCGGGTANAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAG 540
                                                                                                                                                                                                           182 AAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGGAGGTTGTCCA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                              302 AGTGGACCAGCAATGNGCATACAGAGGAGAACTACCAAGGACACCGCACCAATCCTGGAC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 TCTGACGGGTTCTTACTTCATATATAGCAAGCTC-ATATGAAAACAAGCAAGTGGGAGAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 AACAGATICITICICATGCAACGTGAGACACGGAGGGTCTGAAAAATAACTACCTGAAGA 480
                                                                                                        122 AATGCAAGGTCAACAACAACAAGACCTCCCATCACCATCGAGAACCATCTCAAAAATTA 181
                          62 TCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601785835F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4013577 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institutes of Health, Mammalian Gene Collection (MGC)
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Gilbert Smith, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: LLAM9256 row: f column: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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        mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           964 ACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTA 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 02-0CT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Law, Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                   AII58823 595 bp mRNA linear EST 02-0CT ud386412.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone ILMAGE:1448206 5' similar to gb:x67210 M.musculus rearranged immunoglobulin gamma 2b heavy (MOUSE);, mRNA sequence.
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector to vector length is 606
Seq primer: -28ml3 rev2 ET from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 316.
Location/Qualifiers
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source

SATURES

linear

mRNA

/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;

Best Local Sim Matches 566; Query Match

ASE COUNT

Site_2: Sall; transgenic model WNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dr. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
275 c 214 g 179 t

32.0%; Score 507.6; DB 12; Length 939; 82.0%; Pred. No. 3.9e-95; tive 0; Mismatches 119; Indels 19; Gaps 628; Conservative Similarity Query Match BASE COUNT

641 CTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCAC 700

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761 GCCCATTICAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCC 820

821 TAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCAT 880

881 GATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGTGTGAGCGAGGATGACCCAGA 940

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1001 TAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGA 1060

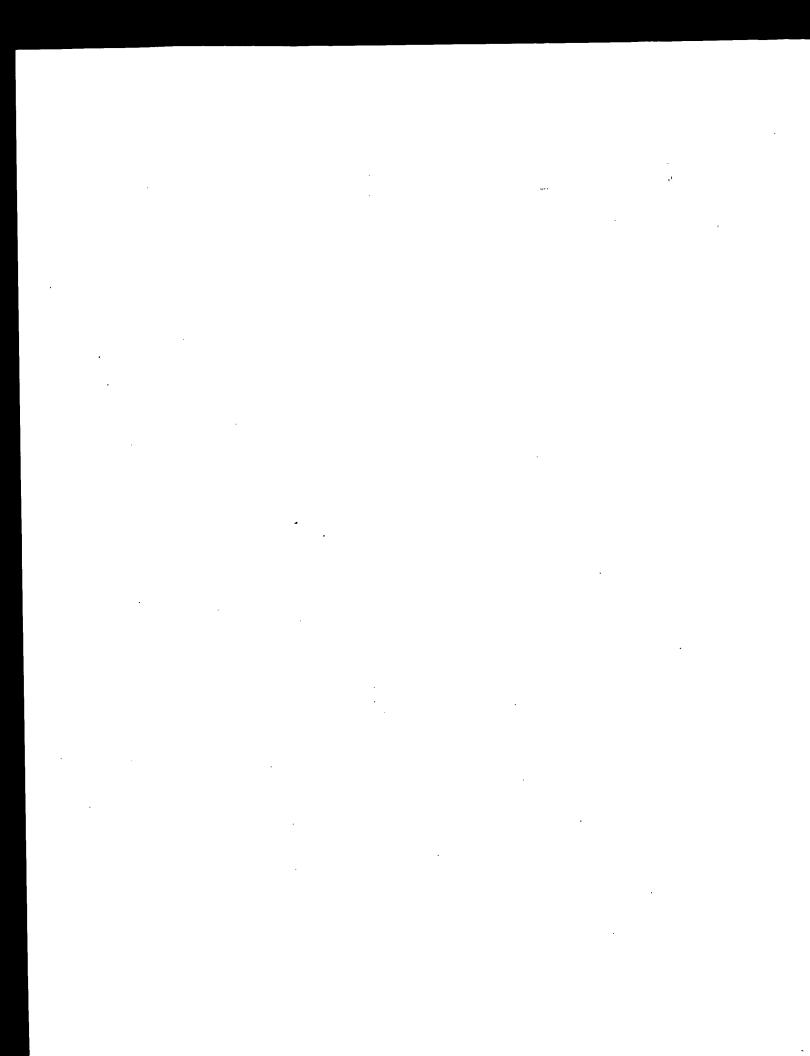
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1241 CAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAA 1300 1301 GGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGCAAGCTCAATAT 1360

1361 GAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTG 1406

earch completed: June 24, 2003, 01:19:55 ob time: 2537.69 secs



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Sequence 81, Appl
Sequence 79, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
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                                                                                                                                                                                                               Sequence 14,
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                                                                                                        June 23, 2003, 20:29:16; Search time 1263.84 Seconds
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/cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:*
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-272-899A-79
US-10-272-899A-79
US-10-272-899A-21
US-10-272-899A-23
PCT-USO2-34420A-21
PCT-USO2-3333A-21
US-10-286-132A-21
US-10-281-479A-21
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US-10-384-933-8
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US-10-429-660-9
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                                                                   AM nucleic - nucleic search, using sw model
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21	637.2	40.1	1401		PCT-US02	PCT-US02-36107-29	Seguence 29. Appl
22	637.2	40.1	1401	10	US-10-2	US-10-292-088-29	•
23	630.8	39.7	1431	7	PCT-US02	-36226-11	Seguence 11, Appl
24	630.8	39.7	1431	10	US-10-2	US-10-291-532-11	Sequence 11, Appl
25	629.2	39.6	1401	Н	PCT-US02	PCT-US02-36107-69	Sequence 69, Appl
26	629.2	39.6	1401	10	US-10-2	92-088-69	Sequence 69, Appl
27	629.2	39.6	1413	٦	PCT-US02	-36107-77	Sequence 77, Appl
28	629.2	39.6	1413	10	US-10-2	US-10-292-088-77	Sequence 77, Appl
29	628.8	39.6	1395	Н	PCT-US02	:-36107-21	Sequence 21, Appl
30	628.8	39.6	1395	10	US-10-2	92-088-21	Sequence 21, Appl
31	628.4	39.6	1425	٦	PCT-US02	:-36107-13	Sequence 13, Appl
32	628.4	39.6	1425	10	US-10-2	92-088-13	Sequence 13, Appl
33	627.6	39.5	1401	Н	PCT-US02	-36107-85	Sequence 85, Appl
34	627.6	39.5	1401	10	US-10-2	92-088-85	Sequence 85, Appl
c 32	627	39.5	3043	_C	US-09-48	8-725B-5987	Sequence 5987, Ap
. 36	625.4	39.4	3043	Ŋ	US-09-48	8-7258-5987	Sequence 5987, Ap
37	624.4	39.3	1413	7	PCT-US02	-36107-61	Sequence 61, Appl
38	624.4	39.3	1413	10	US-10-2	92-088-61	Sequence 61, Appl
39	623	39.2	1416	-4	PCT-US02	-36107-5	Sequence 5, Appli
40	623	39.2	1416	10	US-10-2	92-088-5	Sequence 5, Appli
41	621.4	39.1	1431	10	US-10-2	US-10-225-108A-15	Sequence 15, Appl
42	620.6	39.1	1392	6	0S - 10 - 15	-10-150-475A-7	Sequence 7, Appli
43	619.6	39.0	1413	↤	PCT-US03	PCT-US03-10749-37	Sequence 37, Appl
44	619.6	39.0	1413	10	US-10-4	08-901-37	Sequence 37, Appl
45	618.2	38.9	1449	10	US-10-2	-10-290-703-1	Sequence 1, Appli
					ALTGN	AT.TGWMENTS	
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RESULT	RESULT 1 US-10-144-771-19352	352					

OVERY SYSTEM AND USES THEREOF	Score 919.8; DB 9; Length 8600; Pred. No. 1.2e-230; 0; Mismatches 2; Indels 0; Gaps	CTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGATCCCTGTCC	AGCAGTGTGCACACCTTCCCAGCTCTCTGCAGTCTGGACTCTACACTATGAGCAGCTCA 	GTGACTGTCCCCTCCAGCACCTGGCC <mark>A</mark> AGTCAGACGTCACCTGCAGCGTTGCTCACCCA 	GCCAGCAGCACCACGGTGGACAAAAACTTGAGCCCAGGGGCCCATTTCAACAATCAAC 	CCCTGTCCTCCATGCAAGGAGTGTCA
SULT 1 -10-144-771-19352 Sequence 19352, Application US/10144771 GENERAL INFORMATION: APPLICANT: VENTER, J. Craig TITLE OF INVENTION: HUMAN GENOME DISCOVERY FILE REFERENCE: CLO01321 CURRENT APPLICATION NUMBER: US/10/144,771 CURRENT PILING DATE: 2002-05-15 LENGTH: 8600 LENGTH: 8600 TYPE: DNA ORGANISM: HUMAN -10-144-771-19352	57.9%; 99.8%; vative 0					
RESULT 1 105-10-144-771-19352 Sequence 19352, Appl. GENERAL INFORMATION: APPLICANT: VENTER, TILLE REFERENCE: CLO CURRENT APPLICATION: CURRENT FILING DATE, NUMBER OF SEQ ID NO SEQ ID NO 19352 LENGTHS 8600 SEQ ID NO 19352 LENGTHS BOA TYPE: DNA ORGANISM: HUMAN US-10-144-771-19352	Query Match Best Local Similarity Matches 921; Conser	Oy 540 Db 4863	Oy 600 Db 4923	Qy 660 Db 4983	Qy 720 Db 5043	Qy 780 Db 5103

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990 ACACAAACCCATAGAGAGTTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATC 1049 1051 CCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTG 1110 1170 TACATCTTGCCGCCACCAGCAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTG 1229 1230 GTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAG 1289 1050 CAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAAAGACCTC 1109 991 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGGCCCTC 1050 1110 CCATCACCCATCGAGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTA 1169 931 ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGGGTGGTCAGCGTCCTCACCGTC 990 513 ACTEGITCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACT 572 712 GAGCC------CAAATCTTGTGACAAAGCTCACACATGCCCACCG 750 870 GATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGATGTGAGCGAG 929 811 GACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGACGTGAGCCAC 870 871 GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG 930 273 GCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTAAA 332 333 ATGAACAGTCTGCGAGCTACTGACACACCCATATATTACTGTGCCAGAAATAGAGGGGAT 392 301 ATGAACAGTCTGCAAGCTGATGACACACGCCATGTACTACTGTGCCAGATTTCGCTTTGCT 360 393 ATTIACTATGATITCACTIATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC 452 453 TCCTCAGCCAAAACAACCCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACA 512 415 TCCTCATCC---ACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACC 471 633 ---TCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGT 689 592 TCCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC 651 750 GAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAA 809 810 TGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAG 869 213 GGAAAGGGTCTGGAGTGGCTGGGAGTGATAGGAGTGGTGGAGACACACAGACTATAATGCA 272 121 TGCACTGTCTCTGGATTTTCATTAACCACCTATGGTGTACACTGGTTTCGCCAGCCTCCA 180 573 GIGACITGGAACICIGGAICCCIGICCAGCAGIGIGCACACCIICCCAGCICICCIGCAG 690 CAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCAGCACCACGGTGGACAAAAAAATT á g g ŏ q δŽ g g ò g δλ a δy a δλ g δ 염 g q ŏ g ò ŏ g g δ g d δ ò ò ò ò

1290 GAGAACTACAAGGACACCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGC 1349 1231 AACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 1290 1350 AAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGA 1409 1291 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG 1350 GTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 152 241 GCTCTCATGTCCAGACTGAGCATCAACAAGACACCCAAGAGCCAAGTTTTCTTAAAA 300 513 ACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACT 572 TGCACAGICICTGGIITTCTCATTAACTAGCTATGGIGTACACTGGGTTCGTCAGTCTCCA 212 GGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGAGACACAGACTATAATGCA 272 GCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTAAA 332 ATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACTGTGCCAGAAATAGAGGGGAT 392 ATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTC 452 453 TCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACA 512 reregegeacacacceceregeraceregreaagacracreecegaaccegrace 531 573 GTGACTIGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAG 632 TCCTCATCC --- ACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 471 33 ATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAG 92 1410 CACGAGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAA 1466 50.1%; Score 795; DB 10; Length 1407; 74.4%; Pred. No. 3.8e-198; tive 0; Mismatches 335; Indels 33. APPLICANT: Sandhu, Jasbir TITLE OF INVENTION: Methods For Nucleic Acid Delivery FILE REFERENCE: 2537, 000012 CURRENT APPLICATION NUMBER: US/10/429,660 CURRENT FILING DATE: 2003-05-02 SUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1 Sequence 9, Application US/10429660 GENERAL INFORMATION: Conservative ORGANISM: Homo sapiens Similarity LENGTH: 1407 Best Local Sim Matches 1069; US-10-429-660-9 US-10-429-660-9 TYPE: DNA SEQ ID NO 9 Query Match 333 301 415 ò a οy q ð 셤 윱 ŏ g δŏ g ð 윤 à 8 ά a 용

990 ACACAAACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATC 1049 1050 CAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAAAGACCTC 1109 1110 CCATCACCCATCGAGAGCACCATCTÇAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTA 1169 1051 CCAGCCCCCATCGAGAAACCATCT¢CAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTG 1110 1170 TACATCTTGCCGCCACCAGCAGAGGAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTG 1229 1171 GTCAAAGGCTTCTATCCCAGCGACA‡CGCCGTGGAGTGGGAGGAATGGGCAGCCGGAG 1230 1290 GAGAACTACAAGGACACCGCACCAGACTGGACGGTTCTTACTTCATATAGC 1349 1350 AAGCTCAATATGAAAACAAGCAAGT¢GGAGAAAACAGATTCCTTCTCATGCAACGTGAGA 1409 1291 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG 1350 690 CAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAAACTT 749 750 GAGCCCAGCGGCCCATTTCAACAACCCCTGTCCTCCATGCAAGGAGTGTCACAAA 809 870 GATGTACTCATGATCTCCCTGACACCCCAAGGTCACGTGTGTGGTGGTGTGTGAGCGAG 929 633 ---TCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGT 689 592 TCCTCAGGACTCTACTCCCTCAGCAGCGTGGCCGTGCCCTCCAGCATGGGCACC 651 652 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTT 711 810 IGCCCAGCTCCTAACCTCGAGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAG 869 811 GACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAGGTGAGCCAC 870 532 GIGICGIGGAACICAGGCGCCCIGACCAGGGGGGGIGCACCTICCCGGCIGICCIACAG 591 1410 CACGAGGGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAA 1466 1351 CATGAGGCTCTGCACAACCACTACA¢GCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA 1407 APPLICANT: HANNA, NABIL
APPLICANT: CHINN, PAUL
TITLE OF INVENTION: MODIFIED ANTIBODIES AND METHODS OF PILE REFERENCE: 03703-0280743
CURRENT APPLICATION NUMBER: PCT/USO2/02373
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/254,318
PRIOR FILING DATE: 2001-01-29 Sequence 14, Application PC/TUS0202373 GENERAL INFORMATION: APPLICANT: BRASLAWSKY, GARY R. NUMBER OF SEC ID NOS: 17 PCT-US02-02373-14 RESULT 4 ò g g ŏ g ŏ Q ð g 셤 g Dp q ò ŏ ö δ δ 셤 ò Qγ g ŏ g δy g g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 GCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 ACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACT 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 TCTGGGGGCACAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCCCCGAACCGGTGACG 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 GTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       529 GIGICGIGGAACICAGGCGCCCTGACCAGGGGGGGGGCACCATCCCGGCIGICCTACAG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        633 ---TCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 TCCTCAGGACTCTACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACC 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             649 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAAGTT 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          750 GAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709 GAGCC------CAAATCTTGTGACAAAACTCACACAAGTGTGTGACAAAACTCACACATGCCCACG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         810 TGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAATATCAAG 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 GTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GIGCAGCIGAAGGAGICAGGACCIGGCCIGGIGGCGCCCICACAGAGCCIGICCAICACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 TGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TGCACCGTCTCAGGGTTCTCATTAACCGACTATGGTGTAAACTGGGTTCGCCAGCCTCCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 GGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGAGACACAGACTATAATGCA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 ATGAACAGICTGCGAGCTACTGACACAGCCATATATTACTGTGCCAGAAATAGAGGGGAT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 ATGACCAGTCTGCAAACTGATGACACAGCCAGGTACTACTGTGCCAGA------ 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      349 TGCTATTACGGTAGTAGCCCTTACTTTGACTACTGGGGCCAAGGCACCACTCTCACCGTC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453 TCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGGAGATACA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 TCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACC 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                748 TGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAG 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 ATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACGTC 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 ATGGCTGTTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAG 92
                                                                                                                                                                                                                                                                                                         49.2%; Score 781.2; DB 1; Length 1407; 73.3%; Pred. No. 1.6e-194; tive 0; Mismatches 348; Indels 36; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 73.38 Matches 1056; Conservative
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                               T-US02-02373-14
                                                          LENGTH: 1407
                             SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Donath, Paul
APPLICANT: Pauch, Paul
APPLICANT: Bruce Keyt
TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
TITLE OF INVENTION: USE THEREOR
TITLE OF INVENTION: WONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
TITLE OF INVENTION: USE THEREOR
TITLE OF INVENTION: UNBER: US/10/272,899A
CURRENT FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1290 GAGAACTACAAGGACACCGCACCAGTCCTGGACGCTTCTTACTTCATATAGC 1349
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                                                                                                                                                990 ACACAAACCCATAGAGGGTTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATC 1049
                                                                                                                                                                                                                                                                                                 1050 CAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAAGACCTC 1109
                                                                                                                                                                                                                                                                                                                                                                             988 CTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTC 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1110 CCATCACCCATCGAGAACCATCTCAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTA 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1170 TACATCTTGCCGCCACCAGCAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTG 1229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1228 AACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGC 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1350 AAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGA 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1288 AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATG 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1348 CATGAGGCTCTGCACAACCACTACACGCAGAAGACCTCTCCCTGTCTCCGGGTAAATGA 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1168 GTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAG 1227
928 ACAAAGCCGCGGGGGGGGGGGGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTC 987
                                                                        868 GAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAG 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

48.7%; Score 774; DB 9; Length 1109;
Best Local Similarity 85.1%; Pred. No. 1.2e-192;
Matches 877; Conservative 0; Mismatches 150; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: immunoglobulin cassette sequence Leader-Mu_WT_60 US-10-272-899A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81, Application US/10272899A GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa L.
APPLICANT: Healy, Judith Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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443 AGTCACCGTCTCCTCAGCCAAAACACCCCCATCAGTCTATCCACTGGCCCTGGGTG 502

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Q S		AGICACAGICAGUICAGCCAAAACAACAGCCCCAICGGICIAICCACIGGCCCCIGIGIG 136
δζ	0	TGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGA 562
q	137	GGAGGTACAACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTG
λλ	9	GTCAGTGACTGGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACCTTCCCAGC 622
q	197	AGTGACCTTGACCTGGAACTCTGGCTCCCTGTCCAGTGGTGTGCACACCTTCCCAG
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Ω,	ກີ	CICCIGCAGICIGGCCICIACACCCICAGCAGCICAGIGACIGIAACCICGAACACCIG 31
λ? -	ω ,	CCAAGTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAG
Q	_	AGACCATCACCTGCAATGTGGCCCACCGGCAAGCAGCACCAAAGTGGACAA 37
<u> </u>	₹ (CAACAATCAACCCTGTCCTCCAIGCAAGGAGIG 80
Q	_	AGCCCAGAGTGCCCAT AACACAGAACCCCTGTCCTCCACTCAAAG
<u>۲</u> ۲	0 0	CACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAA 86
ą	ñ	CTTGGGTGGACCATCCGTCTTCATCTTCCCTCC
Δζ	ف	TATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGATGT 922
ą	494	TCAAGGATGTACTCATGATCTCCCTGAGCCCCATGGTCACATGTGTGTG
Κį	923	GAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACAC 982
q	554	SCGAGGATGACCCCAGACCTCCAGATCAGCTGGTTTG
λλ	983	AGCTCAGACACAAACCCATAGAGATTACAACAGTACTATCCGGGTGGTCAGCACCT 1042
q	614	TCAGACACAAACCCATAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCC
λ	4	CCCCATCCAGCACCAGGACTGGATGGCTAGGAGTTCAAATGCAAGGTCAACAACAA 1102
ą	674	CCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGG
Ã	1103	AGACCTCCCATCACCCATCGAGAGCAACCATCTCAAAAATTAAAGGCTAGTCAGAGCTCC 1162
ą	734	CTCCCATCCCCATCGAGAAACCATCTCAAAACCCAGAGGGCCAGTAAGAGCTC
Ϋ́	63	ACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGAAAGATGTCAGTCTCAC 1222
ď	794	NTATGTCTTGCCTCCACCAGCAGAAGAGATGACTAAGAAAGA
Ā		TTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCA 1282
ą	854	CATGATCACAGGCTTCTTACCTGCCGAAATTGCTGTGGACTGGACCAGCAAT
γ	1283	ACAGAGGAGAACTACAAGGACACCGCACCGGTCCTGGACTCTGACGGTTCTTACTT
ā	914	TACAGAGCAAAACTACAAGAACACCGCAACAGTCCTGGACTCTGATGGTTCTTACTTGAT 973
γ	1343	AAAACAAGCAAGTGGGAGAAAACAGATTCCTCAT
q	974	GTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTGCTC 1033
¥	1403	FGAGACACGGTCTGAAAATTACTACTGAAGAAGACCATCTCCCGGTCTCCG
q	1034	SGTCCACGAGGGTCT
λ	1463	1472
ą	1094	TAATAATCT 1103
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APPLICANT: O'Keefe, Theresa L.
APPLICANT: Healy, Judith Jacques
APPLICANT: Newman, Walter
APPLICANT: Ponath, Paul
APPLICANT: Bruce Keyt
TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,
TITLE OF INVENTION: USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     983 AGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTGTGCGGGGGGGTCAGCACCCT 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1043 CCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAA 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 AGTCACCGTCTCCTCAGCCAAAACAACCCCCCATCAGTCTATCCACTGGCCCCTGGGTG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 TGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 GTCAGTGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGC 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       623 TCTCCTGCAGTCTGGACTCTACACTA#GAGCAGCTCAGTGACTGTCCCCTCCAGCACCTG 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 GCCAAGTCAGACCGTCACCTGCAGCGPTGCTCACCCAGCCAGCACCACGGTGGACAA 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 GAAAATTGAGCCCAGAGTGCCCAT---PAACACAGAACCCTGTCCTCCACTCAAAGAGTG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      743 AAAACTTGAGCCCAGCGGGCCCATTT¢AACAATCAACCCCTGTCCTCCATGCAAGGAGTG 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          803 TCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            494 GATCAAGGATGTACTCATGATCTCCCŢGAGCCCCATGGTCACATGTGTGGTGGTGGTGGT 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863 TATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGTGT 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              923 GAGCGAGGATGACCCAGACGTCCAGAȚCAGCTGGTTTGTGAACAACGTGGAAGTACACAC 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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US-10-272-899A-79
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84.9%; Pred. No. 2.1e-191;
tive 0; Mismatches 153;
                                                                                                                                                                                                                 FILE REFERENCE: MT01-244P2RM
CURRENT APPLICATION NUMBER: US/10/272,899A
CURRENT FILING DATE: 2002-10-17
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: 60/392,364
PRIOR APPLICATION NUMBER: 60/392,364
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FASTESEQ for Windows Version 4.0
Sequence 79, Application US/10272899A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 84.99
Matches 874; Conservative
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LENGTH: 1109
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; Sequence 23, Application US/10272899A; GENERAL INFORMATION:
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Ponath, Paul
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TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
TITLE OF INVENTION: USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1034 AGTGGTCCACGAGGGTCTGCACATCACGACTAAGACCATCTCCCGGTCTCTGGG 1093
                                                          1103 AGACCTCCCATCACCCATCGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCC 1162
                                                                                                                                             1163 ACAAGTATACATCTTGCCGCCACCAGCAGAGGTGTCCCAGGAAAGATGTCAGTCTCAC 1222
                                                                                                                                                                                                                                  1223 TTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGGAGTGGACCAGCAATGGGCA 1282
                                                                                                                                                                                                                                                                                                                                                                                                       1343 ATATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAA 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                 974 GTACAGCAAGCTCAGAGTACAAAAGAGCACTTGGGAAAGAGGAAGTCTTTTCGCCTGCTC 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1403 CGTGAGACACGAGGGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGG 1462
                                                                                                                                                                                                                                                                                                                     1283 TACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCAT 1342
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                                                                                                 734 AGCCCTCCCATCCCCCATCGAGAAACCATCTCAAAACCCAGAGGGCCAGTAAGAGCTCC 793
                                                                                                                                                                                         914 TACAGAGCAAAACTACAAGAACACCGCAACAGTCCTGGACTCTGATGGTTCTTACTTCAT 973
                 674 CCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGCATTCAAATGCAAGGTCAACAACAG 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.4%; Score 768.6; DB 9; Length 1027; · 85.1%; pred. No. 3e-191; tive 0; Mismatches 149; Indels 3; Gaps
CURRENT APPLICATION NUMBER: US/10/272,899A CURRENT FILING DATE: 2002-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                       OTHER INFORMATION: mouse IgG2a-WT DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/10272899A GENERAL INFORMATION:
APPLICANT: O'Keefe, Theresa L.
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PRIOR APPLICATION NUMBER: 60/392,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Healy, Judith Jacques
APPLICANT: Newman, Walter
APPLICANT: Ponath, Paul
APPLICANT: Bruce Keyt
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Best Local Similarity 85.18
Matches 871; Conservative
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1230 GTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAG 1289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1110 CCATCACCCATCGAGAGAACCATCTCAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTA 1169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1170 TACATCTTGCCGCCACCAGCAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTG 1229
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                                                                                                                                                                                             690 CAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAACTT 749
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                                                                                            630 CAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGT 689
                                                                                                                          182 CAGTCTGGCCTCTACACCCTCAGCAGCTCAGACGTGTAACCTCGAACACCTGGCCCAGC 241
                                                                                                                                                                                                                                                                                            750 GAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAA 809
                                                                                                                                                                                                                                                                                                                            810 TGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAG 869
                                                                                                                                                                                                                                                                                                                                                                                                                 570 ACTGICACTIGGAACICIGGAICCCIGICCAGCAGTGIGCACACCIICCCAGCTCICCTG 629
                                                                                                                                                                                                                                          242 CAGACCATCACCTGCAATGTGGCCCACCCGGCAAGCAGCACCAAAATGT 301
                                                 122 ACCTIGACCTGGAACTCTGGCTCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTCTCTG 181
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FEATURE:
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APPLICANT: Bruce Keyt

TITLE OF INVENTION: IMMUNOCLOBULIN DNA CASSETTE MOLECULES,

TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF

TITLE OF INVENTION: USE THEREFOR
FILE REFERENCE: MF101-244P2RM
CURRENT PPLICATION NUMBER: U5/10/272,899A

CURRENT FILING DATE: 2002-10-17

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-06-26

NUMBER OF SEQ ID NOS: 110

SOFTWARE: FASTESQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 1027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 ACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 ACCTTGACCTGGAACTCTGGCTCCTGTCCAGTGGTGTGCACACCTTCCCAGCTCTCCCTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630 CAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGT 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  690 CAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAACTT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      750 GAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810 TGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAG 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  870 GATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGGTGGTGGTGGATGTGAGCGAG 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   48.1%; Score 763.8; DB 9; Length 1027; 84.8%; Pred. No. 5.4e-190; Live 0; Mismatches 152; Indels 3;
                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: mouse IgG2a-FcRmut DNA
JS-10-272-899A-23
                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 868; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                FEATURE:
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APPLICANT: LOBUGIO, Albert S.
APPLICANT: LOBUGIO, Albert S.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS FACT TITLE OF INVENTION: APPOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERAPEUTIC AGEN FILE REFERENCE: 21085.002993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
PCT-US02-34420A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1230 GICGIGGGCITCAACCCIGGAGACA¶CAGTGTGGAGTGGACCAGCAATGGGCATACAGAG 1289
                                                                                                                                                                                                                                                         1290 GAGAACTACAAGGACACCGCACCAG¶CCFGGACTCFGACGGTTCTTACTTCATATAGC 1349
                                                                                                                                                                                                                                                                                                                                                                                  1350 AAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGA 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1410 CACGAGGGTCTGAAAAATTACTACCIGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGA 1469
1170 TACATOTTGCCGCCACCAGCAGCAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTG 1229
                             839 CAAAACTACAAGAACACCGCAACAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGC 898
                                                                                                                                                                899 AAGCICAGAGIACAAAAGAGCACITGGGAAAGAGGAAGICITIICGCCIGCICAGIGGIC 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 TCTGCCTGGTGACATTCCCAAGCTGT¢TCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 GAGGCTTAGTGAAGCCTGGAGGGTCCCTGGAACTCTCCTGTGCAGCCTCTGGATTCACTT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 CIGGCCIAGIGCAGCCCICACAGAGCCIGTCCAICACCIGCACAGTCICTGGITTCTCAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 TAACTAGCTATGGTGTACACTGGGTT¢GTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23 TTTTCCTTGTCCTTGTTTTAAAAGGT¢TCCAGTGTGAAGTGATGCTGGTGGAGTCTGGGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.2%; Score 670.6; DB 1; Length 1386; 69.4%; Pred. No. 1.8e-165; Live 0; Mismatches 379; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/USO2/34420A CURRENT FILING DATE: 2002-10-25 PRIOR APPLICATION NUMBER: 60/391,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 202-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 21, Application PC/TUS0234420A; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: The UAB Research Foundation APPLICANT: Zhou, Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhou, Tong
APPLICANT: IChikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oshumi, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           982; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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LENGTH: 1386
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Db 11 Qy 13 Db 12 Qy 13 Qy 13 Qy	Db 12 Qy 14 Db 13	i i ii	APPLICAN APPLICAN TITLE OF TITLE OF TITLE COF CURRENT CURRENT CURRENT PRIOR APP	PRI PRI SOE) SEQ ID NO. TYPE: C ORGANIS FEATURE OTHER I COTHER I POTHER I	Query Mat Best Loca Matches Qy	d Qy do	oy Op	Qy	Qy Db	, so
0 0 0	292 GCATCAGCAAGGACAATTCCAAGAGCCAACTTTTTAAAATGAACAGTCTGCGAGCTA 351	412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACAC 471	532 TGGGATGCCTGGTCAAGGCTACTTCCCTGAGTCAGTGACTTGGAACTTGGAT 591	652 GCAGCTCAGTGACTGCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTG	772 CAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGG 831	892 CACCCAAGGTCACGTGTGGTGGAGTGTGAGCGAGGATGACCCAGACGTCCAGATCA 951			1132 TCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAG 1191	1192 AGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTGGGCTTCAACCCTGGAG 1251 	1252 ACATCAGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCGCAC 1311

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ANT: Buchsbaum, Donald J.
DF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED DF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF SPERENCE: 21085.0029P2
                                                                                                                                                                                372 AGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAAATTACT 1431
                                                                                                                                                                                                                 172 ACATTACTGTGGAGTGGCAGTGGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGC 1231
                                                           312 CAGTCCTGGACTCTGACGGTTCTTACTTCATATAGCAAGCTCAATATGAAAACAAGCA 1371
                                                                                            263 CCATCTCCAGAGACATGCCAAGAACACCCTGTACCTGCAAATGAGGAGTCTGAGGTCTG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 CIGACACAGCCATATATACTGTGCCAGAAATAGAGGGGATATTACTATGATTTCACTT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 TCAGTAGCTATGTAATGTCTTGGGTTCGCCAGACTCCGGAGAAGAGGCTGGAGTCGTCG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 GAGTGATATGGAGTGGTG---GAGACACAGACTATAATGCAGCTTTCATATCCAGACTGA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 CAACCATTAGTAGTGGTGGTAGTTACACTACTATCCAGACAGTGTGAAGGGGGCGTTTCA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTAAAATGAACAGTCTGCGAGCTA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 CIGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 GAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 TITICCTIGICCTIGITITAAAAGGIGICCAGIGIGAAGIGAIGCIGGIGGAGICTGGGG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 69.4%; Pred. No. 1.8e-165; Similarity 69.4%; Pred. No. 1.8e-165; Conservative 0; Mismatches 379; Indels 54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: Description of Artificial Sequence:/Note = INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                        .432 ACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAA 1466
                                                                                                                                                                                                                                                                                                                                                                 352 ATACTGAGAAGACCTCTCCCACTCTCCTGGTAAA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US02/35333A FILING DATE: 2002-11-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2001-11-01
APPLICATION NUMBER: PCT/US01/14151
FILING DATE: 2001-05-02
APPLICATION NUMBER: US 60/201,344
FILING DATE: 2000-05-02
R OF SEQ ID NOS: 102
RAE: PatentIn version 3.0
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APPLICATION NUMBER: US 60/346,402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21, Application PC/TUS0235333A INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NT: The UAB Research Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kimberly, Robert P.
Koopman, William J.
LoBuglio, Albert S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou, Tong
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ð	323	AGGACACGCCATGTATTACTGTGCAAGACGGGG	367
Ā	412 /	ACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAACACAC	471
ą	368 7	SARGGACTACTGGGGCCAAGGCACCACTCACAGTCTCCTCAGCCAAAACGACAC	427
*	472 (CCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTC	531
д	428 (CCCATCTGTCTATCCACTGCCCCTGGATCTGCTGCCCAAACTAACT	487
ъ Q	532 1	IGGGATGCCTGGTCAAGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGAT E 	591
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*	25	GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACGTCACCTGCAGCTTG 7	711
۵	809	STCACCTGCAACGTTG	299
, 4	712 0	CTCACCCAGCCAGCACCACGGGGGACAAAAACTTGAGCCCAGCGGGCCCATTCAA 7 11111 1 1 1 1 1 1 1	771
>-	772	SCTCCTAACCTCGAGG	831
۵	728 #		751
>-	832 6	TCATGATCTCCCTGA	891
۵	752 P	Trcarcricccccaaacccaaggargrecrcaccarracrcra	811
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Ω	12	Jaaggtcacgtgtgttgtggtagacatcagcaaggatgatcccgaggtccagttca	871
ъ с	952 G 872 G	GCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGGATT 1 	1011 931
	1012 A	AGTG	1071
0	932 T	AACAGCACTITCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATG	991
~ c	1072 G 992 G	GCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCATCACCATCGAGAGAACCA 1	1131
_	1132 T		19
•	1052 T		11
	1192 A	AGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAG 1	25
	7 1	saldecchassalaasicasicisaciciscalsalaacasaciicircchs	_
~. c	1252 A	ACMICAGNOTIGAACTIGAACCAGCAATIGGGCATACAGAGAACTACAAGGACACCGCAC 1	-
		TO COLORO MANON CONTROLLO	23
	232	CASICOGARIZIA GAGOGIECITACITECHTA PATRAGARAGETARATA TAGARA ARACAGOR 1 TILLIII	1371 1291
	1372 A	3GGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACT 1	1431
•	1292 A		1351
	432	ACCIGAAGAAGACCAICICCGGGTCTCCGGGTAAA 1466	
•	1352 A	TACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA 1386	

RESULT 11 US-10-286-132 Sequence 21 GENERAL INFO APPLICANT: APPLIC	132A-21 21, Application US/10286132A 21, Application US/10286132A TWI Zhou, Tong TWI Exhou, Tong TWI Exhou, Tong TWI Exhous To
, OTHER US-10-286-	OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct 0-286-132A-21
Query Match Best Local S Matches 982	y Match 42.2%; Score 670.6; DB 9; Length 1386; Local Similarity 69.4%; Pred. No. 1.8e-165; hes 982; Conservative 0; Mismatches 379; Indels 54; Gaps 3;
oy Db	55 TCTGCCTGGTGACATTCCCAAGGTGTCCTATCCCAGGTGCAGCTGAGGAC 114
Qy	115 CTGGCCTAGTGCAGGCCTCACAGAGCTGTGCATCACTGCACAGAGTGTCTGAT 174
Db	83 GAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTT 142
Qy	175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
Dp qu	GTAGTTACACCT
oy da	292 GCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTCTGCGAGCTA 351
Qy 3	352 CTGACACACCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTT 411
Db	323 AGGACACGGCCATGTATTACTGTGCAAGACGGGGGGACTCTATGA 367
Qy 4	412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACA 471
0y	
	CCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAACTAACT
Qy 5	532 TGGGATGCCTGGTCAAGGCTACTTCCCTGAGTCAGTGACTGGGACTTGGAACTCTGGAT 591
pp 4	488 TGGGATGCCTGGTCAAGGGCTATTTC¢CTGAGCCAGTGACGTGAC
Qy 5	592 CCCTGTCCAGGAGTGTGCACACCTTCCCTGCAGTCTGGACTCTACACTATGA 651

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1112 AGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTGAAG 1171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 952 GCTGGTTTGTGAACAACGTGGAAGTACACACACCCCACAGAACCCATAGAGAGATT 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1012 ACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1072 GCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCATCACCATCGAGAGAACCA 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1132 TCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAG 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1052 TCTCCAAAACCAAAGGCAGACGAAGGCTCCACAGGTGTACCACCATTCCACCTCCCAAGG 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1192 AGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAG 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1252 ACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCGCAC 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1372 AGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACT 1431
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712 CTCACCCAGCCAGCAGCACCACGGTGGACAAAAACTTGAGCCCAGCGGGCCCATTTCAA 771
                                                                                                                                                                                                                                                        832 GIGGACCAICCGICTICAICTICCCICCAAAIAICAAGGAIGIACICAIGAICICCCIGA 891
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                                                                                            652 GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTG 711
                                                                                                                                                           608 GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTG 667
                                                                                                                                                                                                                                                                                                                                                    772 CAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGG 831
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TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T TITLE OF INVENTION: AGENTS
FILE REFERENCE: 21085.002906
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2002-06-24
PRIOR FILING DATE: 2001-06-24
PRIOR FILING DATE: 2001-06-24
PRIOR FILING DATE: 2001-06-24
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct US-10-281-479A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 GAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTT 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 TCAGTAGCTATGTAATGTCTTGGGTTCGCCAGAACTCCGGAGAAGAGGCTGGAGTGGGTCG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 670.6; DB 9; Length 1386;
Pred. No. 1.8e-165;
0; Mismatches 379; Indels 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: artificial sequence
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Similarity 69.4%;
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APPLICANT: LOBUGLIO, Albert S. APPLICANT: Buchsbaum, Donald J. TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS

APPLICANT: The UAB Research Foundation Sequence 21, Application US/10281479A GENERAL INFORMATION:

APPLICANT: APPLICANT: APPLICANT: APPLICANT:

-10-281-479A-21

SULT 12

Zhou, Tong Ichikawa, Kimihisa Kimberly, Robert P. Koopman, William J. Oshumi, Jun

APPLICANT: APPLICANT:

; OTHER INFORMATION: Synthetic Construct US-10-275-180A-21	Query Match 42.2%; Score 670.6; DB 10; Length 1398; Best Local Similarity 69.4%; Pred. No. 1.8e-165; Matches 982; Conservative 0; Mi\$matches 379; Indels 54; Gaps 3;	QY 55 TCTGCCTGGTGACATTCCCAAGCTGGTCCTATCCCAGGTGCAGGTGAAGGAGTCAGGAC 114 1 1 1 1 1 1 1 1 1 1	115 CTGGCCTAGTGCAGCCTCACAGAGCTGTCCATCACCTGCACGTCTCTGGTTCTCAT	83 GAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTT 175 TAACTAGCTATGTAACACTGGGTTCGTCAGTCTCCAGGAAGGGTGTGGAGTGGCTGG 1	143 235	203		323 AGGACACGGCCATGTATTACTGTGCAAGACGGGG		428 CCCCAICTGTCTATCCACTGGCCCCTGGGATCTGCTGCCCAAACTAACT	592 592 548	OY 652 GCAGCTCAGTGACTGCCCTCCAGGACCTGGCCAAGTCAGACCGTCACCTGCAGCTTG 711	Qy 712 CTCACCCAGCAGCACCACGGTGGACAAAAAACTTGAGCCCAGCGGGCCCATTCAA 771	QY 772 CAATCAACCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTGGAGG 831 Db 728 AGCCTTGCATATG	QY 832 GTGGACCATCCGTCTTCCATCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGA 891	QY 892 CACCCAAGGTCACGTGTGGTGGTGATGTGAGGAGGATGACCCAGACGTCCAGATCA 951	QY 952 GCTGGTTTGTGAACAACGTGGAAGTA 1	Qy 1012 ACAACAGTACTATCCGGGTGGTCAGCACCCCTCCCCATCCAGCACCAGGACTGGATGAGTG 1071
Db 668 CCCACCCGGCCAGCACCACGAGGTGGACAAGAAATTGTGCCCAGGGATTGTGTGT 727	728 AGCCTTGCATATGTACTCTGCAATATATCAATATGCCCAAGCTAATCTGCAGGGGGGGG	752	0y 892 CACCCAAGGTCACGTGGTGGTGGTGGAGCGAGGATGACCCAGACGTCCAGATCA 951	OY 952 GCTGGTTTGTGAACAACGGAAGTACACACACACACACACA	0y 1012 acaacastarccssgresscreccccarccascacsacsgressgre 1071	QY 1072 GCAAGGAGTTCAAATGCAAGGTCAACGAAGACCTCCCATCACCCATCGAGAAACCA 1131 DD 111111111111111111111111111111111111	OY 1132 TCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAG 1191	2y 1192 AGCAGTTGTCCAGGAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAG 1251	29 1252 ACATCAGTGGGAGTGGACCAGCAATGGGCATACAGAGGAACTACAAGGACACGGCAC 1311	2y 1312 CAGTCCTGGACTCTGACGGTTCTTACTTCATATAGCAAGCTCAATATGAAAACAAGCA 1371	DY 1372 AGTGGGAGAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACT 1431		AESULT 13 15-10-275-180A-21 Sequence 21, Application US/10275180A GENERAL TRYDRAGATON:	APPLICANT: The UAB Research Foundation APPLICANT: Zhou, Tong APPLICANT: Ichikwa, Kimihisa ADDITCANT: Ichikwa, Kimihisa	APPLICANT: KOOPMEN, WILLIAM J. TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS TITLE OF INVENTION: INDOCING LIGAND RECEPTOR AND USES THEREOF FITE PERPERENCE: 31086 0070015	CURRENT APPLICATION NUMBER: US/10/275,180A CURRENT FILING DATE: 2002-10-31 NUMBER OF SEQ ID NOS: 102 SOFFWARE PATANTIN VOSTICATION	SEQ ID NO 21 LENGTH: 1398 TYPE: DIA A CONTROL OF THE CONTROL OF TH	FEATURE: OTHER INFORMATION: Description of Artificial Sequence:/Note =

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                                                                1132 TCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAG 1191
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932 TCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATG 991
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.9%; Score 648.8; DB 10; Length 1392; 68.3%; Pred. No. 9.6e-160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/384,933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/10384933 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Serizawa, Nobufusa
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LOCATION: (58)..(1392)
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LOCATION: (1)..(57)
5-10-384-933-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             995 ATGGCAAGGAGTTCAAATGCAGGGTCAACAGTGCAGCTTTCCCTGCCCCCATCGAGAAAA 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 CTACTGACACACCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCA 408
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CURRENT APPLICATION UNIBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15 Length 1673; Query Match 40.5%; Score 643.6; DB 9; Length 19 Best Local Similarity 66.3%; Pred. No. 2.4e-158; Matches 1021; Conservative 0; Mismatches 479; Indels 1429 ACTACCTGAAGAGCCATCTCCCGGTCTCCGGGTAAA 1466 Van 't Veer, Laura Johanna Van de Vijver, Marc J. Sequence 1932, Application US/10342887 GENERAL INFORMATION: CURRENT FILING DATE: 2003-01-15
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PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710 PRIOR FILING DATE: 2002-05-14 PRIOR APPLICATION NUMBER: 10/172,118 PRIOR FILING DATE: 2002-06-14 Mao, Mao Roberts, Christopher J. APPLICANT: Dai, Hongyue APPLICANT: He, Yudong APPLICANT: Linsley, Peter S. Rene NUMBER OF SEQ ID NOS: 2699 ORGANISM: Homo sapiens Bernards, US-10-342-887-1932 JS-10-342-887-1932 SEQ ID NO 1932 LENGTH: 1673 APPLICANT: APPLICANT: APPLICANT: APPLICANT: a δ qq ŏ a ò 셤

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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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SUMMARIES

Description	Sequence 1, Appli	Sequence 3, Appli		Sequence 3, Appli	Sequence 6, Appli	×.	Sequence 19352, A	Sequence 2, Appli	Sequence 3, Appli		Sequence 14, Appl	Sequence 6, Appli	Sequence 10, Appl	Sequence 11, Appl	Sequence 82, Appl						
·	US-09-770-916-1	US-09-653-755A-3	US-09-653-755A-1	US-07-904-074A-3	743-329-6	JS-08-303-569-6	JS-08-485-686-6	US-09-348-224-6	JS-08-846-658A-6	US-08-846-658B-6	us-09-795-515-6	JS-08-462-767-1	US-60-360-207-19352	JS-07-688-197-2	US-09-629-430B-3	JS-07-688-197-4	US-10-058-120-14	US-07-688-197-6	US-09-584-166B-10	US-09-584-166B-11	PCT-US01-09616-82
ID	.60-SD	0S-09	.60-sn	ns-01-	US-07-7	US-08-3	US-08-4	-60-Sn	ns-08-	ns-08	ns-09	US-08-4	-09-SD	us-07-6	-60-SN	us-07-6	US-10-	us-07-6	-60-SN	-60-SD	PCT-USC
DB	30	25	25	~	æ	7	œ	17	12	12	30	8	80	٣	24	٣	39	٣	22	22	J
Length DB	1588	1389	1365	1645	1570	1570	1570	1570	1570	1570	1570	1581	8600	1462	7528	1437	1407	1427	1431	1431	1676
& Query Match	100.0	68.3	68.1	9.09	59.5	59.2	59.5	59.5	59.1	59.1	59.1.	58.8	57.9	26.7	55.7	50.1	49.2	48.5	48.4	48.4	46.6
Score	1588	1084	1081.2	696	940.8	940.8	940.8	940.8	939.2	939.2	939.2	933	919.8	006	882	795.8	781.2	770.6	768.2	768.2	740.8
Result No.	1	7	e	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	c 20	21

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Sequence 66, Appl
Sequence 1, Appli
Sequence 21, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 190, App
Sequence 190, App
                                                                                                                                                       Sequence 230, App
Sequence 9992, Ap
Sequence 9483, Ap
Sequence 9399, Ap
Sequence 15669, Ap
                                                                                                                                                                                                                          Sequence 5790, Ap
Sequence 5933, Ap
                                Sequence 63, Appl
Sequence 66, Appl
                                                                                                                                                                                                                                                 Seguence 1568, Ap
                                                                                                                                   Sequence 6, Appli
                                                                                                                                                                                                                                                           Sequence 17, Appl
 Sequence 82, App1
             Sequence 4, Appli
                                                                                                                                               Sequence 230, App
                       Sequence 63, Appl
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Frank, Dara W.
APPLICANT: Wiener-Kronish, Jeannine
APPLICANT: Yahr, Timothy L.
APPLICANT: Sawa, Teiji
APPLICANT: Fritz, Robert B.
TITLE OF INVENTION: Method of and compositions for immunization with the TITLE OF INVENTION: Pseudomonas V antigen
FILE REFERENCE: 650053.91487
                                                                                                                                                                                                                          US-09-710-281-5790
US-09-726-174-5933
US-09-726-211-1568
US-09-049-672-17
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US-09-698-010-15669
US-09-699-999-7476
                                                                                                                                                        US-09-925-299-230
US-09-637-886-9992
US-09-652-125A-9483
                                                                                                  US-09-903-327A-1
US-09-760-479-190
US-10-206-008-190
US-09-107-223A-6
                                                                                                                                               PCT-US00-05883-230
                                                                             PCT-US01-14151-21
US-09-815-837-82
                     PCT-US01-09616-63
                                           PCT-US01-09616-66
            US-09-629-430B-4
                                                                                       US-09-613-017-1
                                                                 US-08-480-120-1
                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/770,916 CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: 60/109,952
PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/126,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/448,339
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09770916 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1999-03-30
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 1676
6729
22053
22053
22059
11489
11398
11316
11516
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11610
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NAME/KEY: sig_peptide
LOCATION: (33)...(89)
NAME/KEY: V_region
LOCATION: (57)...(179)
OTHER INFORMATION: FRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (237)..(284)
OTHER INFORMATION: CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (180)..(194)
OTHER INFORMATION: CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: V_region
LOCATION: (195)..(236)
OTHER INFORMATION: FR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
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LOCATION: (237)..(
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 ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1588
                                                                                                                                                                                                                                                                                                                                         -09-770-916-1
                                 684.8
684.8
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670.6
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662
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                                                                                                                                   SEQ ID NO 1
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541 TGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGAACTTGGAACTCTGGATCCCTGTCCA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 TGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTGCTCACCCAG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 CCAGCAGCACCACGGTGGACAAAAACTTGAGCCCAGCGGGCCCATTTCAACAATCAACC 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781 CCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCAT 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TATGGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 CCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 ACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAAACAACACCCCCATCAG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601 GCAGTGTGCACATTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAG 660
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                                                                                                                                                                                             100.0%; Score 1588; 100.0%; Pred. No. 0; Ative 0; Mismatches
                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 1588; Conservative
                              NAME/KEY: V_region
LOCATION: (381)..(425)
OTHER INFORMATION: CDR3
                                                                                                                                NAME/KEY: C_region
LOCATION: (459)..(1466)
                                                                                            OTHER INFORMATION: FR4
NAME/KEV
LOCATION: (285)..(380)
OTHER INFORMATION: FR3
                                                                                 NAME/KEY: V_region LOCATION: (426)..(4
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961	TGAACAACGTGGAAGTACACACACACACACAAACCCATAGAGAGGTTACAACAGTA 1020 -	Ö i
1021	CTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGT 1080 	
1081	TCAAATGCAAGGTCAACAACAAGACCTCCCATCACCTGGGGAACCATCTCAAAA 1140 	a or i
1141	TTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGT 1200 	
1201	CCAGGAAAGAIGICAGICICACITGCCIGGICGIGGGCITCAACCCTGGAGACAICAGIG 1260 	
1261	. TGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGG 1320 	
1321	. ACTCTGACGGTTCTTACTTCATATATAGCAAGCTCAATATGAAAACAAGCAAG	ā 6 î
1381	. AAACAGATTCCTTCTCATGCAACGTGAGACAGGGGTCTGAAAATTACTACCTGAAGA 1440 	ରି ନିର୍ମ
1441	. AGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCACAAAGCTCTCAGGTCCTAA 1500 . 	ā 6√ 7
1501	GAGACACTGGCACCCATATCCATGCATCCCTTGTATAAATAA	ਕੋ ਨੂੰ 1
1561	. GTACCATGTAAAAAAAAAAAAAAAA 1588 	ā <i>6</i> 7 ā

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91 AGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 ATGCAGCTTTCATATCCAGACTGAGGATCAGCAAGGACAATTCCAAGAGCCAACTCTTCT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GCCCGAAGTTCAAGGCCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTACA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                      211 CAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGT---GGTGGAGACACAGACTATA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 ATGGAGAGACCTTGAGTGGATTGGAGGTATTAATCCTTACTATGGTGGTTCTATCTTCA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAAAATGAACAGTCTGCGAGCTACIJGACACAGCCATATATTACTGTGCCAGAAATAGAG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 TGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAAGGGCTG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 CCGTCTCCTCAGCCAAAACAACACCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAG 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 CAGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 ATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 ATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAG 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        808 AATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCA 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 928 AGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACGCTC 987
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                                                                                                                                                                                                                                                          2 AGTCCAGCTGCARCAGTCTGGACCTGGACTGGTGAAGCCTGGGGCTTCAGTGATGAT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 TGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACCACCTTCCCAGCTCTCC
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                                                                                                                                                         21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: chain of recombinant antibody with 3'-histidine OTHER INFORMATION: tag sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1389;
                                                                                                   Score 1084; DB 25; Length
Pred. No. 1.1e-255;
1; Mismatches 156; Indels
                                                                                                   68.3%;
87.2%;
                                                                                                                                                         Matches 1218; Conservative
                                                                                                                              Local Similarity
                                                   JS-09-653-755A-3
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OTHER INFORMATION: Description of Artificial Sequence:cDNA for heavy

ORGANISM: Artificial Sequence

APPLICANT: LaMarche, Arthur
APPLICANT: Jelinek, Thomas
TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for
TITLE OF INVENTION: Phosphotyrosine-Containing Proteins

Sequence 3, Application US/09653755A GENERAL INFORMATION:

IS-09-653-755A-3

APPLICANT: Eisinger, Dominic P. APPLICANT: Stiles, Lynn

CURRENT APPLICATION NUMBER: US/09/653,755A

FILE REFERENCE: 724650-3

CURRENT FILING DATE: 2000-09-01 NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3

1389

TYPE: DNA

SULT 3

SEC ID NO 1 TYPE: DNA

1456	GTGA 13	qq	
18.5 18.5	GACACGAGGCTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAAT 140 GACACGAGGGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAAT 136:	Qy	44 TCCATCACCTGCACAGTCTCTGGTTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGT 20
135 Description of the property		qa	O AAACTCTCCTGTGCAGCCTCCGGATTCACTTTCAGTAGTTATGCCATGTCTTGGGTTCGC 24
10 10 10 10 10 10 10 10		Qy	04 CAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGAGTGATAGAGTGGTGGAGACACAGAC
10 10 10 10 10 10 10 10	AESULT 4 13-07-904-074A-3	oy.	TATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTC 32
1	equence 3, Application US/07904074A GENERAL INFORMATION:	qa	TATGTAGACAGTGTGAAGGGCCGATTCACCGTCTCCAGAGACAATGCCAGGAACATCCTG 36
By 1971 1972	APPLICANT: John E. Shively APPLICANT: Rainer Fischer ADDITCAND: A DOT FORMER	Qy	TTCTTTAAAATGAACAGTCTGCGAGGTACTGACACACACA
March Marc	AFFILCANI: ROLL BY ALL BY AFFILCANI: ROLL BY BY AFFILCANIS OF TAXABLE B	qa	TACCTGCAAATGAGCAGTCTGAGGTGTGAGGACACGGCCATGTATTACTGTGCAAGA 42
St. Propriet Propriet St. Prop	TITLE OF INVENTION: Chimeric Anti-CEA Antibody NUMBER OF SEQUENCES: 10	QY Db	AGAGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCA
11	CORRESPONDENCE ADDRESS: ADDRESSES: City of Hope GEDERE: 1500 Back housets	Qy	GTCACCGTCTCCTCAGCCAAAACAACCCCCCATCAGTCTATCCACTGGCCCCTGGGTGT
December	Simming and Daile Kodu CITY: Duarte STATE: California	qa	
Proceedings Procession Pr	COUNTY: United States of America ZIP: 91010-0269	Qy	GGAGATACAACTGGTTCCTCCGTCACTCTGGGATCCCTGGTCAAGGGCTACTTCCCTGAG 56
SYSTEM: Name SYST	le Density 5 1/4"	qa	GGAGATACAACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAG
Microsoft (8) 10 10 10 10 10 10 10 1	-DOS (R) Version	Qy	64 TCAGTGACTGTGGACTTGGATCTGGATCCTGTCCAGCAGTGTGCACACTTCCCAGCT 62
10 10 10 10 10 10 10 10	SOFTWARE: Microsoft (R) CURRENT APPLICATION DATA:	qa —	8 ccagraaccrraaccraaacrcraarccrarccaaracrarcarc
State Marker Name	APPLICATION NUMBER: US/07/904,074A FILING DATE: 19920615 CLASSIFICATION: 530	oy do	CTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTCACTGTCCCTCCAGCACCTCGG
100 100	PRIOR APPLICATION DATA: .None ATTORNEY/AGENT INFORMATION:	2	CCAAGTCACCACCACCACCACCACCACCACCACCACCACCACCAC
The process	NAME: Irons, Edward S. REGISTRATION NUMBER: 16,541	. qo	CCCAGCCAGTCCATCATGTGGCCCACCCGCAAGCACCACCAAGGTGGAAAG 77
10.00 10.0	REFERENCE/DOCKET NUMBER: None TELECOMMUNICATION:	QY	AAACTTGAGCCCCAGGCCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGT 8
0	TELEFAUNE: (202) 785-0938 TELEFAX: (202) 785-5351 TELEX: 4400R7 IM MSH	qq	
Decirity 1.64 11 11 11 11 11 11 11	NFORMATION FOR SEQ 1D NO: 3: SEQUENCE CHARACTERISTICS:	Qy	04 CACAAATGCCCAGCTCCTAACCTCGAGGTGGACCATCCGTCTTCATCTTCCTCCAAAT 86
December	LENGTH: 1645 TYPE: NUCLEIC ACID STRANDFONDES: 64.0.1.5 Stranded	qq	22CAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCTTCATCTTCCCTCCAAAG 87
Discrete and papel cable by a decaded and a concentration of the papel cable by a decaded and a decaded	JAMANDENESS: SINGLE SLAMMED TOPOLOGY: Unknown MOLECULE TYPE: Nucleic Acid	. OY	64 ATCAAGGATGTACTCATCATCATCCCTGACACCCAAGGTCACGTGTGGTGGATGTG 9
PE: Not Applicable When the control of the control	HYPOTHETICAL: Not Applicable ANTI-SENSE: Not annicable	gg i	ov atcaassatstacticalsaticticcissasciccicalastictics services and a services of the services o
ON ON ON ON ON ON ON ON	PRAGMENT TYPE: Not Applicable ORIGINAL SOURCE: Synthetically Prepared	λλ Pd	4 AGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGAACAACA 98
ONE INFORMATION: None 60.6%; Score 963; DB 3; Length 1645; CONSERVAÇÃO COACCAGGACTGAGAGATTACAACAGTACTCTCGGGTGGTCACTCTCCGGTGGTCACTCTCCGGTGGTCACTCTCCGGTGGTCACTCTCCGGTGGTCACTCTCCGGTGGTCACTCTCCGGTGGTCACACACTCTCCGGTGGTCACACACA	IMMEDIATE SOURCE: Synthetically Prepared POSITION IN GENOME: None	i č	TO TO THE CONTROL OF
60.6%; Score 963; DB 3; Length 1645; ilarity 77.6%; Pred. No. 6.8e-226; Conservative 0; Mismatches 320; Indels 30; Gaps 3; TCAGAGCATGGGTGTCTTGGCTGGTGAAGGGTTCAAATGCAAGACTAAAAAAAA	one INFORMATION:	QG QG	GCTCAGACACACAAACCCATAGAGAATACAACAGACTATCCGGGGTGGTCAGCCCCC 104 GCTCAGACACACACAAACCCCATAGAGAATACAACAGTATTCTCGGGGTGGTCTTTTTTTT
Pred. No. 5.88-225; Dear N	60.6%; Score 963; DB 3;	δδ	CCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAA 11
OY 1104 GACCICCATCACCCATCACAGAGACCATCTCAAAATTAAAGGGTAGTCAGAGGTCCA 116	Pred. No. 6.8e-226; 0; Mismatches 320; Indels 30; Gaps	q0 :	CCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAA 111
OY 1164 CAAGTATACATCTTGCCGCCACCAGGAGGAGTTGTCCAGGAAAGATGTCAGTCTCACT 122	C 83	dg dg	ACCITCCATCATCATCGAGAGAACCATCTCAAAATTAAAGGGCTAGTCAGAGCTCCA 116 GACCTCCCAGCGCCATCGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCA 117 GACCTCCCAGCGCCATCGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCA 117
	12 12	δy	CAAGTATACATCTTGCCGCCACCAGCAGAGTGTCCCAGGAAAGATGTCAGTCTCACT 122

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                                      1224 TGCCTGGTCGTGGCCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCAT 1283
                                                                            1240 TGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAACGGGAAA 1299
                                                                                                                   1284 ACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATA 1343
                                                                                                                                                         1300 ACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATG 1359
                                                                                                                                                                                               1344 TATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAAC 1403
                                                                                                                                                                                                                                      1404 GTGAGACACGAGGGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGT 1463
                                                                                                                                                                                                                                                                                                                                                         1464 AAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCATATCCAT 1523
                                                                                                                                                                                                                                                                                                                                                                                               1480 AAATGAGCTCAGCACCCACAAAACTCTCAGGTCCAAAGAGACACCCACACTCATCTCCAT 1539
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                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CARP-0009
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/743,329
FTI.ING DATE: 19910917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/07743329 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1570 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Philadelphia
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81 GTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGC 140
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                                                                                                                                                                                       36;
                                                                                                                          59.2%; Score 940.8; DB 3; Length 1570; 77.2%; Pred. No. 1.9e-220; tive 0; Mismatches 322; Indels 36;
                                                                                                                                                                                         Matches 1210; Conservative
                        mat_peptide
98..1444
                                                                                                                                                              Best_Local Similarity
                           NAME/KEY:
LOCATION:
                                                                             US-07-743-329-6
                                                                                                                                          Query Match
FEATURE:
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NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFRENCE/DOCKET NUMBER: CARP-0009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1570 base pairs

single

STRANDEDNESS:

linear

TOPOLOGY:

MOLECULE TYPE: CDNA

nucleic acid

ATTORNEY/AGENT INFORMATION:

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1038 ACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1097
                                                                     1098 AACAAAGACCTCCCATCACCCATCGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGA 1157
                                                                                                                                                                      1158 GCTCCACAAGTATACATCTTGCCGCCACCAGCAGCAGTTGTCCAGGAAAGATGTCAGT 1217
                                                                                                                                                                                                                           1218 CTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAAT 1277
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mat_peptide 98..1444

NAME/KEY: LOCATION: LOCATION:

US-08-303-269-6

41..1444

NAME/KEY: CDS

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81 GTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGC 140
                                                                                                                                                                                                                                                               141 CIGICCATCACCIGCACAGICICTGGFTICTCATTAACTAGCTATGGTGTACACTGGGTT 200
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59.2%; Score 940.8; DB 7; Length 1570; 77.2%; Pred. No. 1.9e-220; Live 0; Mismatches 322; Indels 36;
                                              Matches 1210; Conservative
                            Best Local Similarity
     Query Match
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Woodcock Washburn Kurtz Mackiewicz & Norris

One Liberty Place - 46th Floor

Philadelphia USA

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COUNTRY:

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET:

NUMBER OF SEQUENCES:

Sequence 6, Application US/08303569
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies

S-08-303-569-6

ESULT 6

SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM: MEDIUM.TYPE: Floppy disk

APPLICATION NUMBER: US/08/303,569

APPLICATION NUMBER: US 07/743,329

CLASSIFICATION: 424 PRIOR APPLICATION DATA:

FILING DATE:

FILING DATE: 17-SEP-1991

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                        918 GATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 977
                                                                                                                                                                                                                                                                                                             798 GAGIGICACAAAIGCCCAGCICCIAACCICGAGGGIGGACCAICCGICIICAICIICCCI 857
                                                                                                                                           784 ------CAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCT 835
                                                                                                                                                                                         858 CCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCCAAGGTCACGTGTGTGGTGGTG 917
                                                                                                                                                                                                                                      836 CCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCATAGTCACATGTGTGGTGGTGGTG 895
738 GACAAAAACTTGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAG 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Adair, John R. APPLICANT: Athwal, Diljeet S. APPLICANT: Emtage, John S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1578 AAAAAAA 1585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -08-485-686-6
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Woodcock Washburn Kurtz Mackiewicz & Norris

NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:

ADDRESSEE:

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149 GIGAAGAIGICCIGCAAGGCIICIGGCIACACCIIIACIAGGIACACGAIGCACIGGGIA 208
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                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
APPLICATION NUMBER: US/08/485,686
FILMS DATE: 07-JUN-1995
One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/743,329
FILING DATE: 17-SEP-1991
ATTORNEY AGENT INFORMATION:
NAME: HOHENSCHULZ, Liza D.
REGISTRATION NUMBER: 33,712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CARP-0009
                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1570 base pairs
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LOCATION: 98..1444
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STRANDEDNESS: single
                                                                                                                                 COMPUTER READABLE FORM:
                         Philadelphia
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                                                                                                                                                                                               COMPUTER:
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                                                                              COUNTRY:
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  STREET:
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4 ACCACTCTCACAGTCTCCTCAGCCAAAACAACAGCCCCATCGGTCTATCCACTGGCCCCT	8 GGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTC	8 CCTGAGTCAGTGACTGGACTTCGGATCCCTGTCCAGCAGTGTGCACCTTC	8 CCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGC	8 ACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTGCTCAGCCCAGCCAG	38 GACAAAAACTIGAGCCCAGGGGCCCATITCAACAATCAACCCCTGTCCTCCATGCAAG	98 GAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCT	58 CCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTG 	18 GATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA	8 CACACAGCTCAGACAAACCCATAGAGATTACAACAGTACTATCCGGGTGGTCAGC	ACCTCCCCATCCAGCACCAGGACTGGATGAGGGAGGAGGAGTTCAAATGCAAGGTCAACCAAC	AACAAAGACCTCCCATCACCCATGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGA	8 GCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAG	8 CTCACTTGCCTGGTCGTCGTCGACCCTGGAGACATCAGTGTGGAGTGGACCAGCAAT	8 GGGCATACAGAGGAGAACTACAAGGACACCGCACCAGCAGCTCCTGGACCGGTTCTTAC	8 TTCATATATAGCAAGCTCAATATGAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCA 	B TECAACGTGAGACCACGAGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCT	8 CCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCAT 	8 ATCCATGCATCCTTGTATAAATAAAGCATCCAGCAAAGCCTGGTACCATGTAAAAAAAA
43	49	55.55	618	678	73	79	83	91.8	97.	1038	109	115	1218	1278	1338	1398	1458	1518

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.2%; Score 940.8; DB 17; Length 1570; 77.2%; Pred. No. 1.9e-220; tive 0; Mismatches 322; Indels 36;
                                                                                                       US-09-348-224-6

Sequence 6, Application US/09348224

GENERAL TRFORMATION:
APPLICANT: Jollieffe, Linda Kay
APPLICANT: Jollieffe, Linda Kay
APPLICANT: Joln Robert Allan
APPLICANT: Athwal. Diljeet Singh
TITLE OF INVENTION: CD3 Specific Recominant Antibody
FILE REFERENCE: CARPO066
CORRENT FAPLICATION NUMBER: US/09/348, 224
CURRENT FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 08/116, 247
EARLIER APPLICATION NUMBER: 08/116, 247
EARLIER APPLICATION NUMBER: 07/743, 377
EARLIER PILING DATE: 1991-10-04
NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.1
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Matches 1210; Conservative
1578 AAAAAAA 1585
                                     1556 AAAAAAA 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (41)..(1444)
US-09-348-224-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Mouse
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                        918 GATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 977
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                                                                                  618 CCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGC 677
                                                                                                           738 GACAAAAACTIGAGCCCAGCGGCCCATITCAACAATCAACCCTGTCCTCCAIGCAAG 797
                                                                                                                                                                                                                                                                                                      734 GACAAGAAATTGAGCCCAGAGGGCCC----ACAATCAAGCCCTGTCCTCCATG---- 783
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81 GTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGC 140
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                                                                                                                                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Sequence 6, Application US/08846658A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE, DOCKET UNMBER:
TELECOMMUNICATION INFORMATION:
TELEFAN: (215) 568-3100
TELEFAN: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                  APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
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98..1444
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COMPUTER READABLE FORM:
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US-08-846-658A-6
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378 AGAAATA(11 1 1 1 1 1 1 1 1 1	TTTACTATGATTCACTTATGCCATGGACTACTGGGTCAAGGA 4	37 33	
38 34 98	7		
98	ACCTCAGTCACCGTCTCCTCAGCCAAAACAACCCCCCATCAGCTCTATCCACTGGCCCCT 4	97	
	GGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGCTACTTC 5:	57 53	
558 CCTGAGT(554 CCTGAGC	CCTGAGTCAGTGACTGGGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACTTC 6:	617 613	
618 CCAGCTCT 614 CCAGCTGT	CCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGÍCCCCTCCAGC 6. 	677 673	
678 ACCTGGCC 674 ACCTGGCC	ACCTGGCCAAGTCACACCGTCACCTGCAGCGTTGCTCACCCAGCCAG	37	
738 GACAAAA 734 GACAAGA	GACAAAAAACTTGAGCCCCAGGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAG 79 	97	
798 GAGTGTC2	GAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCT 8:	57 35	
858 CCAAATA1 836 CCAAAGA1	CCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGGTGTGTGGGTGG	17 95	
918 GATGTGAC 896 GATGTGAC	GATGTGAGCGAGGAFGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 97 	77 55	
978 CACACAGC 956 CACACAGC	CACACAGCTCAGACACAAAACCCATAGAGAGTTACAACAGTACTATCCGGGTGGTCAGC 1(037 015	
1038 ACCTCCC 1016 GCCTCCC	ACCETCCCCATCCAGGACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGGTCAAC 10	097	
1098 AACAAAGA 1076 AACAAAGA	AACAAAGACCTCCCATCACCCATCGAGAGACCATCTCAAAAATTAAAGGGCTAGTCAGA 11	157 135	
1158 GCTCCACA 1136 GCTCCACA	GCTCCACAAGTATACATCTTGCCGCCACCAGCAGCAGTTGTCCAGGAAAGATGTCAGT 12 	217	
1218 CTCACTTC 1196 CTGACCTG	CTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAAT 12 	277	
1278 GGGCATAC 1256 GGGAAAC	GGGCATACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTAC 13 	337	
1338 TTCATATA 1316 TTCATGTA	TTCATATATACCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCA 13 	397 375	
1398 TGCAACGT 	TGCAACGTGAGACACGAGGGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCT 14 	435	

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1436 CCGGGTAAATGAGCTCAGCACCCACAAAAACTCTCAGGTCCAAAAAAGAGACACCCCACACTCAT 1495
                                                                                                          1458 CCGGGTAAATGAGCTCAGCACCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCAT 1517
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris STREET: One Liberty Place - 46th Floor CIIY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,658B
FILING DATE: 01-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAMME: TIVIJILO, DOTEON TATKO
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: 35,719
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Humanised Antibodies NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                       ; Sequence 6, Application US/08846658B; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Adair, John R. APPLICANT: Athwal, Diljeet S. APPLICANT: Emtage, John S.
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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Matches 1209; Conservative
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LOCATION: 98..1444
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STRANDEDNESS: single
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41..1444
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LOCATION:
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141 CTGTCCATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGACACTGGGTT 200
                          269 ACTAATTACATTCAGAAGTTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCAGC 328
                                                                                                                                                                                                                                                                                                          378 AGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGA 437
                                                                                                                                                                                                                                                                                                                                                                                                                           389 AGA------TATTATGATGATCATTACTGCCTTGACTACTGGGGCCAAGGC 433
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                                                                                             201 CGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGA---GTGATATGGAGTGGTGGAGAC 257
                                                                                                                                         209 AAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCCGTGGTTAT 268
                                                                                                                                                                                         258 ACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGC 317
                                                                                                                                                                                                                                                                                  318 CAACTCTTCTTAAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACTGTGCC 377
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1436 CCGGGTAAATGAGCTCAGCACCACAAAACTCTCAGGTCCAAAGAGACACCCACACTT 1495
                       1196 CTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAAC 1255
                                                                     1278 GGGCATACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTAC 1337
                                                                                                               1256 GGGAAAACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTAC 1315
                                                                                                                                                             1338 TTCATATATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCA 1397
                                                                                                                                                                                                                                                     1398 TGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGAACATCTCCCGGTCT 1457
                                                                                                                                                                                                                                                                                                                                           1458 CCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCAT 1517
E: Woodcock Washburn Kurtz Mackiewicz & Norris
One Liberty Place - 46th Floor
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  APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILLING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09795515 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 6:
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MEDIUM TYPE: Floppy disk
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nucleic acid
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CORRESPONDENCE ADDRESS:
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CITY: Philadelphia
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81 GTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGC 140 141 CTGTCCATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGGTATGGTGTACACTGGGTT 200 209 AAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCCGTGGTTAT 268 89 GTCCACTCCCAGGTCCAGCTGCAGTCTGGGGCTGAACTGGCAAGACCTGGGGGCCTCA 148 149 GTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTACTAGGTACACGATGCACTGGGTA 208 201 CGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGA---GTGATATGGAGTGGTGGAGAC 257 258 ACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGC 317 269 ACTAATTACATTCAGAAGTTCAAGGACAAGGCCACATTGACTACAGACAAATCCTCCAGC 328 318 CAACTCTTCTTTAAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACTGTGCC 377 329 ACAGCCTACATGCAACTGAGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCA 388 378 AGAAATAGAGGGGATATTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGA 437 389 AGA------TATTATGATGATGATCATTACTGCCTTGACTACTGGGGCCAAGGC 433 ACCTCAGTCACCGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCT 497 734 GACAAGAAAATTGAGCCCAGAGGCCC----ACAATCAAGCCCTGTCCTCCATG---- 783 784 -----CAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCT 835 GGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTC 557 558 CCTGAGTCAGTGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCCACCTTC 617 618 CCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGC 677 614 CCAGCIGICCIGCAGICIGACCICIACACCICAGCAGCICAGIGACIGIAACCICGAGC 673 674 ACCTGGCCCAGCCAGTCCATCACCTGCAATGTGGCCCCACCCGGCAAGCAGCACCAAGGTG 733 857 836 CCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGTGGTGGTGGTG 895 896 GATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 955 21 CTCCATCAGAGCATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGT 80 738 GACAAAAAACTTGAGCCCAGCGGCCCATTTCAACAATCAACCCTGTCCTCCATGCAAG 797 918 GATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 977 29 CTCTGACTCAACATGGAAAGGCACTGGATCTTTCTACTCCTGTTGTCAGTAACTGCAGGT 798 GAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCT 36; Length 1570; Score 939.2; DB 30; Length Pred. No. 4.8e-220; . 0; Mismatches 323; Indels _ _ _ _ _ 59.18; Matches 1209; Conservative Best Local Similarity NAME/KEY: LOCATION: IS-09-795-515-6 498 438 ٩ ŏ ð ą ð ā Þα ہٰ ہ

TITLE OF INVENTION: COMPLEX HYBRID PROTEINS, METHOD FOR TITLE OF INVENTION: PREARING THEM, THEIR APPLICATIONS AS DIAGNOSTIC AGENT, TITLE OF INVENTION: AGENT INTENDED FOR THERAPEUTIC USE OR AS REAGENT WHICH CAN NUMBER OF SEQUENCES: 4 1016 GCCTCCCCATCCAGCACCAGGACTGGATGAGGGGAAGGATTCAAATGCAAGGTCAAC 1075 1436 CCGGGTAAATGAGCTCAGCACCCACAAAAACTCTCAGGTCCAAAGAGACACCCACACTCAT 1495 ACCCTCCCCATCCAGCACCAGGACTGCATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1097 1098 AACAAAGACCTCCCATCACCCATCGAGAGCATCTCCAAAAATTAAAGGGCTAGTCAGA 1157 1158 GCTCCACAAGTATACATCTTGCCGCCACCAGCAGGCAGTTGTCCAGGAAAGATGTCAGT 1217 1278 GGGCATACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTAC 1337 1338 TTCATATATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCA 1397 1398 TGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCT 1457 CACACAGCTCAGACACAAACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGC 1037 1458 CCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCAT 1517 1518 ATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAGCCTGGTACCATGTAAAAAAA 1577 PatentIn Release #1.0, Version #1.25 3: Bell, Seltzer, Park & Gibson Post Office Drawer 34009 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,767 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 1, Application US/08462767 GENERAL INFORMATION: Duncanel, Frederic Gillet, Daniel Menez, Andre APPLICANT: Boulain, Jean C. Floppy disk North Carolina COMPUTER READABLE FORM: CORRESPONDENCE ADDRESS: 1556 AAAAAAA 1563 1578 AAAAAAA 1585 Charlotte MEDIUM TYPE: FILING DATE: 28234 ADDRESSEE: SOFTWARE: APPLICANT: APPLICANT: APPLICANT: COUNTRY: US-08-462-767-1 qq g ŏ g δ g ŏ a ò 셤 a ò δ οχ ò ŏ

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1327 GATGGTTCTTACTTCATGTACAGCAAGCTGAGAGTGGAAAAGAAGAACTGGGTGGAAAGA 1386
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                               726 AGCACCACGGTGGACAAAAACTTGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGT 785
                                                                                                                                                 745 AGCACCAAGGIGGACAAGAAATIGAGCCCAGAGGGCCC----ACAAICAAGCCCIGI 798
                                                                                                                                                                                                                                               799 CCTCCATG------CAAATGCCCAGCACCTAACCTCTTGGGTGGACCATCCGTC 846
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         Sequence 19352, Application US/60360207 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 GTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGT 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 GCAAGCGGTAATACTAAGTACAATGAGAACTTCAAGGGCAAGGCCACATTGACTGTAGAC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 TICCCAAGCIGICTCTATCCCAGGIGCAGCIGAAGCAGICAGGACCIGGCCTAGIGCAG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 GGAACTGCAGGTGTCCATTGCCAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 CCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 TICTCATAGAGCCICCATCAGAGCATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 AAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGAACTCTGGATCCCTGTCCAGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.8%; Score 933; DB 8; Length 1581;
Best Local Similarity 76.6%; Pred. No. 1.6e-218;
Matches 1207; Conservative 0; Mismatches 335; Indels 33; Gaps
                                         APPLICATION NUMBER: US 08/016,024 FILING DATE: 10-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                 NAME: Linker Jr., Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                              TELEFAX: 704-334-2014
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         LENGTH: 1581 base pairs
                                                                                                                                                                                                             704-377-1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: sig_peptide LOCATION: 61..117
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                     PRIOR APPLICATION DATA:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                    nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61..1467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5223 GTCACGTGTGTGGTGGTGGATGTGAGCGAGGATGACCCCAGACGTCCAGATCAGCTGTTT 5282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5283 GTGAACAACGTGGAAGTACACACACCTCAGACACAAACCCATAGAGGGATTACAACAGT 5342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1020 ACTATCCGGGTGGTCACCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAG 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5403 ITCAAATGCAAGGTCAACAACAAGACCTCCCATCACCATCGAGAACCATCTCAAAA 5462
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                                                                                                                                                                                                                                                                                                                                                                                                                      600 AGCAGTGTGCACACCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCA 659
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                                                                                                                                                                                                                                                                         0; Gaps
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CURRENT APPLICATION NUMBER: US/60/360,207
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 19352
                                                                                                                                                                                                                                                                       Matches 921; Conservative
                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                            ORGANISM: HUMAN
JS-60-360-207-19352
                                                                                               8600
                                                                                                                          TYPE: DNA
                                                                                               LENGTH:
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89 CCAGGIGCAGCIGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCAT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 GAGCATGGCTGTCTTGGGGCTGCTCTTCTGCTGGTGACATTCCCAAGCTGTGTCTATC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Gaps
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                                                                                                                                                                                                                                                                                             - LEGAL AFFAIRS
                                                                                                                                                                             APPLICANT: FOUSER, LYNETTE A
APPLICANT: SWANBERG, STEPHEN L
TITLE OF INVENTION: RECOMBINANT 3F8-TYPE ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPALLLY
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,197
FTTING DATE: 19910419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cuery match 56.7%; Score 900; DB 3; I Best Local Similarity 77.2%; Pred. No. 2.1e-210; Matches 1133; Conservative 0; Mishatches and
                                                                                                                                                                                                                                                                                       ADDRESSEE: GENETICS INSTITUTE, INC.
ADDRESSEE: DEPARTMENT
                     5763 AAGACCATCTCCCGGTCTCCGGG 5785
1440 AAGACCATCTCCCGGTCTCCGGG 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCDANIELS, PATRICIA A
REGISTRATION NUMBER: 33,194
REPERBROKEZ-POCKET NUMBER: GI 5166
TELECOMMUNICATION INFORMATION:
TELEPHONE: 876-1170 EXT. 405
                                                                                                                                                                                                                                                                                                                               STREET: 87 CAMBRIDGEPARK DRIVE CITY: CAMBRIDGE
                                                                                                 RESULT 14
US-07-688-197-2
; Sequence 2, Application US/07688197
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1462 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
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ORIGINAL SOURCE:
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LOCATION:
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US-07-688-197-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE:
                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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1229 GGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCCATACAGA 1288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            989 GACACAAACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCAT 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1049 CCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCT 1108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 709 CGAGCCTAGAATACCCAAGCCCAGTACCCCCCAGGTTCTTC--------750
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                                                                                                                                                                                                                                                                                                                                                                    329 TAAAATGAACAGTCTGGGAGCTACTGACACCACATATATTACTGTGCCAGAAATAGAGG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 -------TCACTACGGCTATGCTTTGGACTACTGGGGTCAAGGAACCTCAGTCAC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 CGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      409 CGTCTCCTCAGCTACAACAACAACACCCCATCTGTCTATCCCTTGGTCCCTGGCTGCAGTGA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         569 GACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 AACTGTAAAATGGAACTATGGAGCCCTGTCCAGCGGTGTGCGCACAGTCTCATCTGTCCT 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               749 TGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAA 808
                           121 CACTTGCACTGTCTCTGGGTTTTCAGTAACCAATTATGGTGTACACTGGGTTCGCCAGCC 180
                                                                                                   209 TCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGAGACACACAGACTATAA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AAAAATGAACAGTCTGCAAATTGATGACACAGCCATGTACTACTGTGCCAGTCGGGGGGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 GGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCAC 448
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1351 GCATGAGGCTCTCCATAACCACCACACAGAAGAACCTGTCTCGCTCCCCTGGTAAATG 1410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1546 TGTGAACGCCGCGGACACGGCTGTGTATTACTGTGCGAGAGTTATTACTAGGGCGAGTCC 1605
1171 GGTCACCAACTTCTTCTCTGAAGCCATCAGTGGGAGGGGAAAGGAACGGAGAACTGGA 1230
                                                           1289 GGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATAG 1348
                                                                                                                      1231 GCAGGATTACAAGAACACTCCACCCATCCTGGACTCAGATGGGACCTACTTCCTCTACAG 1290
                                                                                                                                                                                    1349 CAAGCTCAATATGAAAACAAGCAAGTGGGAAAAACAGATTCCTTCTCATGCAACGTGAG 1408
                                                                                                                                                                                                                                            1291 CAAGCTCACTGTGGATACAGACAGTTGGTTGCAAGGAGAAATTTTTACCTGCTCCGTGGT 1350
                                                                                                                                                                                                                                                                                                          1409 ACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATG 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1306 ACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGGTGT 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence; cDNA US-09-629-430B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: FLT-3-Ligand-Encoding Polynucleotide as TITLE OF INVENTION: Polynucleotide-Based Vaccine Enhancer FILE REFERENCE: 1530.0130001.
CURRENT APPLICATION NUMBER: US/09/629,430B
CURRENT FILING DATE: 2000-07-31
                                                                                                1469 AGCTCAGCACCACAAAGCTCTCAGGTC 1496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09629430B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hermanson, Gary George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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Sequence 2, Appli Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 25, Appl

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RESULT 1 US-09-795-515-6	; Sequence 6, Application US/09795515	; Publication No. US20030039645A1	; GENERAL INFORMATION:			; APPLICANT: Emtage, John S	; TITLE OF INVENTION: 1	; NUMBER OF SEQUENCES:	; CORRESPONDENCE ADDRESS:	: • ADDRESSEE: Woodcocl	; STREET: One Libert	; CITY: Philadelphia	; STATE: PA	; COUNTRY: USA	; ZIP: 19103	; COMPUTER READABLE FORM:	; MEDIUM TYPE: Floppy disk	; COMPUTER: IBM PC compatible	; OPERATING SYSTEM: PC-DOS/MS-DOS	; SOFTWARE: Patentin	; CURRENT APPLICATION DATA:	; APPLICATION NUMBER: US/09/795,51	; FILING DATE:	; CLASSIFICATION:	; PRIOR APPLICATION DATA:	; APPLICATION NUMBER: 08/846,658	; FILING DATE: 01-MAY-1997	; ATTORNEY/AGENT INFORMATION:	; NAME: Trujillo, Doi	; REGISTRATION NUMBER: 35,719	; REFERENCE/DOCKET NUMBER: CARP-0057	; TELECOMMUNICATION INFORMATION:	; TELEPHONE: (215) 568-3100	: TELEFAX: (215) 568-3439	222	; INFORMATION FOR SEQ ID NO:	; INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:	; INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: : LENGTH: 1570 base pairs	INFORMATION FOR SEQ ID N SEQUENCE CHARACTERISTIC LENGTH: 1570 base p TYPE: nucleic acid	: INFORMATION FOR SEQ ID NO ; SEQUENCE CHARACTERISTIC; ; LENGTH: 1570 base pa ; TYPE: nucleic acid ; STRANDEDNESS: single	; INFORMATION FOR SEQ ID SEQUENCE CHARACTERIST]; LENGTH: 1570 base I TYPE: nucleic acti; STRANDEDNESS: singlification of the strength of the s	: INFORMATION FOR SEQ ID SEQUENCE CHARACTERIST; : LENGTH: 1570 base if TYPE: nucleic acid; : STRANDEDNESS: singit TOPOLOGY: linear
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MOLECULE TYPE: CDNA
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1076 AACAAAGACCTCCCAGCGCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGA 1135
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                                     896 GATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 955
918 GATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 977
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                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/815,837 CURRENT FILING DATE: 2001-03-22
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PRIOR APPLICATION NUMBER: US 60/264,003
PRIOR FILING DATE: 2001-01-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 82, Application US/09815837 Patent No. US20020082411A1 GENERAL INFORMATION:
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Arimilli, Subhashini
Wang, Aijun
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84.7%; Pred. No. 6.8e-219;
tive 0; Mismatches 137; Indels 18;
                                                                 OTHER INFORMATION: Description of Artificial Sequence:pCB223
OTHER INFORMATION: recombinant MHC class II heterodimer
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                                                           1416 GGTCTGAAAAATTACTACCTGAAGAAGACATCTCCCGGTCTCCCGGGTAAATGAGC 1471
                                                                                           458 AGCCAAAACAACACCCCCATCAGTC#ATCCACTGGCCCCTGGGTGTGGAGATACAACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Immune Medators and Related Methods FILE REFERENCE: 014058-005670US
CURRENT APPLICATION NUMBER: 02/09/815,837
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/191,274
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2000-05-15
PRIOR FILING DATE: 2001-01-23
                                                                                                                                                                                                                                                                           ; Sequence 63, Application US/09815837
; Patent No. US20020082411A1
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Carter, Darrick
APPLICANT: Zhu, Shirley
APPLICANT: Arimilli, Subhashini
APPLICANT: Wang, Ajun
APPLICANT: Corixa Corporation
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APPLICANT: Li, Erguang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
TITLE OF INVENTION: GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                1959 GGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCATCACC 2018
1599 CACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAAACTTGAGCCCAG 1658
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                                                                                                                                                818 TCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACT 877
                                                                                                                                                                                                                                                    878 CATGATCTCCCTGACACCCAAGGTCACGTGTGTGTGGTGGTGTGTGAGCGAGGATGACCC 937
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41.7%; Score 662; DB 9; Length 1516;
Best Local Similarity 66.5%; Pred. No. 1.7e-194;
Matches 1048; Conservative 0; Mismatches 455; Indels 73; Gaps
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CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 33 SOFTWARE: FastSEQ for Windows Version 4.0
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DELIVERY
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APPLICANT: Nemerow, Glen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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LENGTH: 1516
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       1773 CATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGATGTGAGCGAGGATGACCC 1832
                                                                              998 CCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCA 1057
                                                                                                                                                                                                                                                         1058 GGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAAGACCTCCCATCACC 1117
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                                                       0; Gaps
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APPLICANT: Arimilli, Subhashini
APPLICANT: Arimilli, Subhashini
APPLICANT: Arimilli, Subhashini
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Immune Medators and Related Methods
FILE REFERENCE: 014058-0056700S
CURRENT APPLICATION NUMBER: US/09/815,837
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PRIOR APPLICATION NUMBER: US 60/204,249
PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 60/264,003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 66, Application US/09815837 Patent No. US20020082411A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
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LENGTH: 2059
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	GTGCCAGAAATAGAGGGGATATTACTATGACTTATGCCATGGACTACTGGGGTC [ACTTCCTGAGTCAGTGACTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACAA	CCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAG	CCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCT	TGGTGGATGTGAGCGAGGATGACCCAGATCAGCTGGTTGTGAACAACGTGGTTGTGAACAACGTGGTTGTGAACAACGTGGTTGTGAACAACGTGGTTGTGAACAACGTGGTGGTAGATGATGAGGATTACAGCTGGTTTGTAGATGATGGTGGAACGCTGGTTGTAGATGATGGTGGAACCCATAGAGGATTACAACAGAACGGTGGTTACAACAGTACTATCCGGGTGGTTGTAACAACAGTACTATCCGGGTGGTTGTTACAACAGTACTATCCGGGTGGTTGTTACAACAGTACTATCCGGGTGGTTACAACAGTACTATCCGGGTGGTTACAACAGTACTATCCGGGTGGTGGTGAACAGTACTATCCGGGTGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCCGGGTGGTGAACAGTACTATCAACAGTACTATCCGGGTGGTGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAAC		
9 9 5 1 1 1	373 371 433 398 493 458	553 518 613 578	673 638 733 698	793 750 853 782	4 4	902 1033 962 1093	1022 1153 1082 1213

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G (GGAATGGGCAGCCAGCGGAGAACTACAAGAACACTCAGCCCATCATGGACACAGATGGCT
δλ i	CTTACTTCATATATAGAAGCTCAATATGAAAACAAGCAAG
QQ (262 CITACTICGICTACAGCAAGCICAAIGIGCAGAAGAACAACIGGGAGGCAGGAAATACTT 132
d Db	1993 TCTVATGCARGGTAGGAGGGTCTGAAAATTACTGACTGAAGAGGACCATCTCCC 1452
δλ	1453 GGTCTCCGGGTAAATGAGGTCAGGAGCCACAAAGGTCTCAGGTCCTAAGAGACACTGGCA 1512
Dp	1382 ACTCTCCTGGTAAATGATCCCAGTGTCCTTGGAGCCCTCTGGTCCTACAGGACTCTGTCA 1441
Qy	1513 CCCATATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAGCCTGGTACCATGTAAA 1572
Db	1442 CCTACCTCCACCCTCCC-TGTATAAATAAAGCACCTAGGCACTGGGACCCTGCAA 1500
Qy	1573 AAAAAAAAAAAA 1588
qq	1501 TAAAAAAAAAAAA 1516
RESULT US-09- ; Sequ	SULT 6 -09-925-299-230 Sequence 230, Application US/09925299 Publication No. US20030040617A9
; GENE	RMATION: Rosen et al.
; TIT ; FIL	VENTION: Nucleic Acids, Proteins and Antibodies NCE: PA102
; CUR	RENT APPLICATION NUMBER: US/09/925, 299 RENT FILING DATE: 2001-08-10
; PRI	OR APPLICATION NUMBER: PCT/US00/05883 OR FILING DATE: 2000-03-08
; PRI	OR APPLICATION NUMBER: 60/124,270 OR FILING DATE: 1999-03-12
MON :	NUMBER OF SECTION STATES OF SE
SEQ :	EQ ID NO 230
; 。	NGTH: 1798 DF: DNA
OR	ATTL: John Sapiens PRAMICE: HOMO Sapiens
NA .	
35 	LOCATION: (1) OTHER INFORMATION: n equals a,t,q, or c
NA .	ture
35	OTHER TRY PROMATION: n equals a,t,g, or c
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; OT ;	OTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc_feature
35	ION: (31)
NAN .	OTHER INFORMATION: N equals a, t, g, or c NAME/KEY: misc_feature
35	LOCATION: (501) OTHER INFORMATION: D equals a.t.g. or c
, NA	KEY: misc_feature
, DOCALL ; OTHER US-09-925-	HER INCOMATION: n equals a,t,g, or c 925-299-230
Query Ma	Y Match 41.2%; Score 554.6; DB 9; Length 1798;
Matc	1013; Conservative 10;
Qy	55 TCTGCCTGGTGACATTCCCAAGCTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
Dp	170 THEFT

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949 TCAGCTGGTTTGTGAACAACGTGGAAGTACACACACGCTCAGACACAAACCCATAGAGAGG 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                          350 CAGTTATATSRTATGATGGAAGTAATAATACTATGCAGACTCCGTGAAGGGCCGATTCA 409
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                                                                              230 GAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCSTCTGGATTCACCT 289
                                                                                                                                                                 175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
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115 CTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
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1407 CTCCCGTGCTGGACTCCGACGCTCCTTCTTCCTCTAYAGCAAGCTCACGTGGACAAGA 1466
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                                                                                                                                                                                                                                                                                     1369 GCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATT 1428
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                                                  1287 GGGAKGAGMTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCA 1346
                                                                                             1249 GAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCG 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA102
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CURRENT FILING DATE: 2001-08-10
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PRIOR FILING DATE: 2000-03-08
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Patent No. US20020055627A1
GENERAL INFORMATION:
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LOCATION: (1798)
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55	TCTGCCTGGTGACATTCCCAAGCTGTGCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC	
115	CTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174	
175 290	TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGTCTGGAGTGGCTGG 234 	
235 350	GAGTGATATGGAGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGACTGA 291 	
292	GCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTAAAATGAACAGTCTGCGAGCTA 351 	
352	CTGACACAGCCATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTT 411 	
412	ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACA 471 	
472	CCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGACACTGGTTCCTCGTGACTC 531	
532	TGGGATGCCTGGTCAAGGCTACTTCCCTGAGTCAGTGACTGGGACTTGGAACTCTGGAT 591 	
592	CCCTGTCCAGCAGTGCACACCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTA 648	
649	TGAGCAGCTCAGTGACTGCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCG 708 	
709	TTGCTCACCCAGCCAGCAGCACCACGGTGGACAAAAACTTGAGCCCAGCGGGCCCATTT 768	
769	CAACAATCAACCCTGTCCTCCATGCAAGGGTGTCACAAATGCCCAGCTCCTAACCTCG 828CAAATCTTGTGACAAAACTCACAATGCCCACGTGCCCAGCACCTGAACTCC 926	
829 927	AGGGTGGACCATCCGTCTTCCTCCTCCAAATATCAAGGATGTACTCATGATCTCCC 888 	
989	TGACACCCAAGGTCACGTGTGTGGTGGATGTGAGGAGGATGACCCAGACGTCCAGA 948 	
949	TCAGCTGGTTTGTGAACAACGTGGAAGTACACAGCTCAGACACAAACCATAGAGAGG 1008 	
1009	ATTACAACAGTACTAGCGGGTGGTCACCACCCTCCCCATCCAGCACCAGGACTGGATGA 1068 	
1069	GTGCCAAGGAGTTCAAATGCAAGGTCAACAAGAAGACCTCCCATCACCCATCGAGAGA 1128 	

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1227 CCATCTCCAAAGCCAAAGGGCAGCCCCGAAACCAGGTGTACACCCTGCCCCATCCC 1286
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1129 CCATCTCAAAAATTAAAGGGCTAGTCAGAGGCTCCACAAGTATACATCTTGCCGCCACCAG 1188
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
ITILEONT: Takahashi, Tohru
ITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216, 484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499, 662
PRIOR APPLICATION NUMBER: US/09/499, 662
PRIOR APPLICATION NUMBER: US/09/499, 662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 8
LENGTH: 1392
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LOCATION: (58)..(1392)
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; LOCATION: (1)..(57)
US-10-216-484-8
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FEATURE:
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                                                                                                                              80 GGGCTGAGCTTGTGAAGCCTGGGGCTTCAGTGAAGCTGTCCTGCAAGGCTTCTGGCTACA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 CCACATTGACTGTAGACACATCCTCCAGCACACACTACATGCAGCTCAGCAGCCTGACAT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 CTACTGACACACCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            320 CTGAGGACTCTGCGGTCTATTACTGTGCAAGAAATAGGG------ACTATAGTAACA 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409 CTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   469 CACCCCCATCAGCTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529 CTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   589 GATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTA 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709 TTGCTCACCCAGCCAGCACCACCACGTGGACAAAAACTTGAGCCCAGCGGGCCCATTT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671 TTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCCAGGGATTGTGGTT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            769 CAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCG 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            889 TGACACCCAAGGTCACGTGTGGTGGTGGTGGAGCGAGGATGACCCAGACGTCCAGA 948
                                                                                                                                                                                             172 CATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGC 231
                                                                                                                                                                                                                                                             140 CCTTCACCAGCTACTGGATGCAGTGGGTAAAACAGAGGCCTGGACAGGGCCTTGAGTGGA 199
                                                                                                                                                                                                                                                                                                                               232 TGGGAGTGAT---ATGGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGAC 288
                                                                                                                                                                                                                                                                                                                                                                                           200 TCGGAGAGATTGATCCTTCTGATAGCTATACTAACTACATCAAAGGTTCAAGGGGCAAGG 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 TGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTCTGCGAG 348
                                                               112 GACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCT 171
20 TCCTCTTCTTGGTAGCAACAGCTACAGGTGTCCATTCTCAGGTCCAACTGCAGCAGCCTG 79
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1189 CAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCTG 1248
                                                               1115 AGGAGCAGATGGCCAAGGATAAAGTCAGTCTGACCTGCATGATAACAGACTTCTTCCCTG 1174
                                                                                                                                  1249 GAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCG 1308
                                                                                                                                                                                              1309 CACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGCAAGCTCAATATGAAAACAA 1368
                                                                                                                                                                                                                                                                                                                                                                                                1369 GCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAAATT 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1295 GCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACATGAGGGCCTGCACAACC 1354
                                                                                                                                                                                                                                                                                                                                    1235 AGCCCATCATGAACACGAATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAGA 1294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 CAGITATAIGETAGAAGAAGTAATAAATACTAIGCAGCAGCICCGIGAAGGGCCGAIICA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTCACCT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 GAGTGATATGGAGTGGTGGAGACACAGACTATAATGCAG---CTTTCATATCCAGACTGA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 CCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCCG 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 TITICCTCGTTGCTCTTTTAAGAGGTGTCCAGTGTCAGGTGCAGCTGGTGGAGTCTGGGG 82
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Similarity 68.5%; Pred. No. 2.6e-187;
75; Conservative 0; Mismatches 407; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1429 ACTACCTGAAGAGACCATCTCCGGGTCTCCGGGTAAA 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1355 ACCATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAA 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/153,382 CURRENT FILING DATE: 2002-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/10153382 Publication No. US20030086930A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 975; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-153-382-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Sequence 31, Application US/09859053

18-09-859-053-31

GENERAL INFORMATION: USCUZZOLOGISTAL
GENERAL INFORMATION: USCUZZOLOGISTAL
APPLICANT: Tacuka, Katsunari
APPLICANT: Tacuka, Katsunari
APPLICANT: Tacuka, Katsunari
APPLICANT: Hori, No. USZOLOZOLOZOSBALuaki
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 05501-079001
CURRENT APPLICATION NUMBER: US/09/659,053
CORRENT FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 4.0 55 TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114 116 TITICCTIGITGCTATATTAGAAGGTGTCCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGG 175 296 CAGCTATTGGTACTGCTGGTGACACATACCAGGCTCGTGAAGGGCCGATTCACCA 355 529 CTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTG 588 115 CTGGCCTAGTGCAGGCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174 175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGGAAAGGGTCTGGAGTGGCTGG 234 236 TCAGTAGCTACGACATGCACTGGGTCCGCCAAGCTACAGGAAAAGGTCTGGAGTGGGTCT 295 235 GAGTGATATGGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCA 294 355 ACACAGCCATATTACTGTGCCAGAATAGAGGGGATATTACTATG-----ATTTCA 408 416 ACACGCCTGTGTATTACTGTGTAAGAGATAATAGGAAGGTGACCCACGAGCACTACTACT 475 409 CTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAAACAA 468 469 CACCCCCATCAGTCTATCCACTGGCCCCTGGGTGGAGATACAACTGGTTCCTCCGTGA 528 536 AGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGGGG 595 295 TCAGCAAGGACAATTCCAAGAGCCAACTCTTCTTTAAAATGAACAGTCTGCGAGCTACTG 354
 Query Match
 40.1%;
 Score
 636.6;
 DB 10;
 Length 1708;

 Best Local Similarity
 66.2%;
 Pred.
 No. 1.4e-186;

 Matches 1014;
 Conservative
 0;
 Mismatches 474;
 Indels 43;
 = OTHER INFORMATION: n = A, T, C or G LOCATION: (1507)...(1708) US20020102658A1 LOCATION: (94)...(1503) NAME/KEY: 3'UTR NAME/KEY: sig_peptide LOCATION: (94)...(150) NAME/KEY: misc_feature LOCATION: (1)...(1708) ORGANISM: Homo sapiens LUCCATION: (1)...(93)
NAME/KEY: CDS NAME/KEY: 5'UTR LENGTH: 1708 US-09-859-053-31 SEQ ID NO 31 TYPE: DNA FEATURE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               983 AGTICAACIGGIACGIGGACGCGIGGAGGIGCAIAAIGCCAAGACAAAGCCACGGGAGG 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1006 AGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1043 AGCAGTTCAACAGCACGTTCCGTGTGGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGC 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1103 TGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGA 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1126 GAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCAC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1163 AAACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCAT 1222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1223 CCCGGGAGGAGGATGACCAAGAACCAGGTCAGCCTGACTGCCTGGTCAAAGGCTTCTACC 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     826 TCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCT 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        886 CCCTGACACCCAAGGTCACGTGTGTGGTGGTTGTGAGCGAGGATGACCCAGACGTCC 945
596 CCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAG 655
                                                                                                                                                                                   646 CTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCA 705
                                                                                                                                                                                                                                                716 CCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCA 775
                                                                                                                                                                                                                                                                                                             706 GCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAAACTTGAGCCCAGCGGGCCCA 765
                                                                                                                                                                                                                                                                                                                                                                          776 ACGIAGAICACAAGCCCAGCAACACCCAAGGIGGACAAGACAGIIGAGCGCAAAIG---- 830
                                                                                                                                                                                                                                                                                                                                                                                                                                    766 TITCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACC 825
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118 TITICCTIGITGCTATATAGAAGGIGICCAGIGIGAGGIGCAGCIGGAGICTGGGG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409 CITATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAA 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CTGGCCTAGTGCCAGCCCTCACAGGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 TCAGTAGCTACGACATGCACTGGGTCCGCCAAGCTACAGGAAAAGGTCTGGAGTGGGTCT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 GAGTGATATGGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCA 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 AGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTCCGAGAGCACAGGG 597
                                                                                                               APPLICANT: Tezuka, Katsunaıı APPLICANT: Hori, No. US20020102658Aluaki TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 475; Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 40.0%; Score 635; DB 10; Length 1673; Best Local Similarity 66.2%; Pred. No. 4.3e-186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 43 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/859,053 CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
Sequence 35, Application US/09859053 Patent No. US20020102658A1 GENERAL INFORMATION:
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NAME/KEY: 3'UTR
LOCATION: (1509)...(1673)

NAME/KEY: sig_peptide

LOCATION: (96)...(152)

US-09-859-053-35
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                                                                                          APPLICANT: Tsuji, Takashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(95)
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: 5'UTR
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GENERAL INFORMATION:

946 AGATCAGCTGGTTTGTGAACAACGTGGAAGTACACAGCTCAGACACAAACCCATAGAG 1005 1006 AGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGA 1065 1066 TGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCATCACCCATCGAGA 1125 1426 ATTACTACCTGAAGAAGACCATCTCCGGGTTCAGGGTAAATGAGCTCAGCACCACAAA 1485 985 AGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGG 1044 1126 GAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCAC 1185 1246 CTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACA 1305 1285 CCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCA 1344 1306 CCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATAGCAAGCTCAATATGAAAA 1365 1345 CACCTCCCATGCTGGACTCCGACGCCTCCTTCTTCCTACAGCAAGCTCACCGTGGACA 1404 1366 CAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAA 1425 1405 AGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACA 1464 1525 GC-CCCCCCCCCCCCAGGCTCTCGGGGTCGCGTGGCTTGGCACGTACCCCGTGTAC 1583 GATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAG---TCTGGACTCTACA 645 646 CTATGAGCAGCTGAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCA 705 706 GCGTTGCTCACCAAGCAGCACCACGTGGACAAAAAACTTGAGCCCAGCGGGCCCA 765 766 TITCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACC 825 826 TCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCT 885 CCCTGACACCCCAAGGTCACGTGTGTGTGGTGGATGTGAGCGAGGATGACCCAGACGTCC 945 925 CCCGGACCCCTGAGGTCACGTGCTGGTGGACGTGAGCCACGAAGACCCCGAGGTCC 984 -------TIGIGICGAGIGCCCACCGIGCCCAGCACC---AC 864 = = = = = = = = = = 1546 ATCCAGCAAAGCCTGGTACCATGTAAAAAA 1576

4; 55 TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114 229 GCCTGGGAGTGATATGGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGAC 288 203 GGCTTGGAAACATTTTTCGAGTGACGAGAAGTCCTTCAGTCCTTCTCTGAAGAGCAGAC 262 289 TGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTCTGCGAG 348 349 CTACTGACACACCATATATTACTGTGCCAGAAATAGAGGG---GATATTTACTATGATT 405 406 TCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAA 465 115 CTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174 466 CAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCG 525 643 ACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCT 702 APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: ANUFACTURE AND THERAPEUTIC USE THEREOF 175 TAA-----CTAGCTATGGTGTACACPGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGT 526 TGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACT 586 CTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAG---TCTGGACTCT 503 CGGCCCTGGGCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACT 40.0%; Score 634.6; DB 10; Length 1428; 67.6%; Pred. No. 5.2e-186; Indels 0; Mismatches 429; FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376 PRIOR FILING DATE: 1995-06-07 Patentin Ver. 2.1 965; Conservative NUMBER OF SEQ ID NOS: 27 ORGANISM: Homo sapiens ; LOCATION: (1)..(1425) US-09-740-002-17 Best Local Similarity NAME/KEY: CDS 1428 SEQ ID NO 17 TYPE: DNA Query Match · FEATURE: SOFTWARE: Matches g δ δy à οy g δy ŏ qq g g òχ ŏ ŏ g δλ qq δ a

703 GCAGCGTTGCTCACCCAGCCAGCAGCACCACGTGGACAAAAAACTTGAGCCCAGCGGGC 762

Sequence 17, Application US/09740002 Patent No. US20020001798A1

IS-09-740-002-17

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FEATURE:
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1022 GCCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAAGGCCTCCCAGCCCCCCATCG 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1183 CACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCA 1242
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                                                                                                                                                                                                                                                                                                                                                                                                                                      782 AACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 841
                                                                                                                                                                                                                                                                                                883 TCTCCCTGACACCCAAGGTCACGTGTGTGGTGGATGTGAGCGAGGATGACCCAGACG 942
                                                                                                                                                                                                                                                                                                                            683 GCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCC------ 734
                                                                              763 CCATITICAACAATCAACCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCCAGCTCCTA 822
                                                                                                                                                                                     823 ACCTCGAGGGTGGACCATCCTTCTTCTTCCTCCAAATATCAAGGATGTACTCATGA 882
                                                                                                                                   735 ------CAAATCTTGTGACAAAACTCACATGCCCACCGTGCCCAGCACCTG 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1423 AAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGA 1469
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NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/10124905
Patent No. US20020166136A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 699 Prince Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
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41 CTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 AGTIGITGGAATGGITTACAACAACTGGTTCGATGTCTGGGGCCCCGGGAGTCCTGGTCAC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 CGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      429 CGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCTAAGAG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       509 TACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 GAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 CTCTGGTTTCTCATTAA---CTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 GGGGCTGGAGTGGGAGTTTCTATAGTAGTAGTGGGGAACACCTACTACAACCCCTC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 TITCAIAICCAGACTGAGCAICAAGAAAATICCAAGAGCCAACTCTICITIAAAAI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 GAACTCTATGACCGCCGCGGACACGCCCGTGTATTACTGTGTGAGAGATCGTCTTTTTC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 67.6%; Pred. No. 7.9e-185;
Matches 976; Conservative 0; Mismatches 432; Indels 36:
                    PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                 012712-131
                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION: NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                       US/10/124,905
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                                                                                                                                                                                                                               703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1431 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                              CURRENT APPLICATION DATA APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                      703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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                                                                                                                                                                                                     FILING DATE:
                                                                                                   FILING DATE
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LOCATION:
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                              SOFTWARE:
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'n	5,60	;	
, a	549	GACGGTGTCGTGGAACTCAGGCCCTGACAGGTGCACACCTTCCCGGCTGCTCT	
λλ	629	GCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCC 685	
đ	609	ACAGTCCTCAGGACTCTACTCCCTCAGCAGGTGGTGCTGCCCTCCAGCAGCTTGGG 668	
¥ 4	686	AAGTCAGACCGTCACCTGCAGCGTTGGTCACCCAGCCAGC	
2		CACCCASACCIACAICISCAACSISAAICACAGCCAGCAACACCAAGGIGGACAAGAA 728	
<u></u> 42	729	ACTITAGGCCCAGGGGGCCCATTTCAACAATCAACCCTGTCCTCCATGCAAGGAGGTCA 805	
λï	806		
ā	768	ACCGTGCCCAGCACCACCAGCAACTCCTGGGGGGGACCGTCAGTCTTCCCCCCAAAACC 827	
Ϋ́ q	866	CAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGATGTGAG 925	
Ņ.	926		
۾	888	CCACGAAGACCCTGAAGTTCAACTGGTACGTGGTGGTGGAGGTGCATAATGC 947	
¥	986	TCAGACACAAAACCCATAGAGAGTTACAACAGTACTATCCGGGTGGTCAGCACCCTCCC 1045	
ą	948	CAAGACAAAGCCGCGGGGGGGGGGGGGGTGTACAACAGCGTGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGT	
¥	1046	CATCCAGCACCACGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGACTCAACAAAGA 1105	
ą	1008	CGTCCTGCACCAGGACTGGCTGAATGGCAAGGACTACAAGTGCAAGGTCTCCAAAGAAGC 1067	
γ q	1106	CCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAAGGGCTAGTCACAGCTCCACA 1165 	
٨	1166	AGTATACATCTTGCCGCCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTG 1225	
Д	1128	GGTGTACACCCCGCCATCCCGGGATGAGCTGACCAGGACCAGGTCAGCCTGACCTG 1187	
λ.	1226	CCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGACTGGACCAGCAATGGGGATAC 1285	
Q	1188	CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCGTGGGAGAGCAAGCA	
γ	1286	AGAGGAGAACTACAAGGACACCGCAGTCCTGGACTCTGACGGTTCTTACTTCATATA 1345	
q	1248	GGAGAACAACTACAAGACCACGCCTCCCGTGCTGGGACGCCTCCTTCTTCTTCTTCTTA 1307	
λ	1346	TAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGT 1405	
a	1308	CAGCAAGCTCACCGTGGACAAGAGCAGGGGGAACGTCTTCTCATGCTCCGT 1367	
٨	1406	GAGACACGAGGGTCTGGAAAAATTACTACCTGAAGAAGACCATCTCCGGGTCTCCGGGTAA 1465	
Ф	1368	GATGCATGAGGCTCTGCACAACCACAGAAGAGCCTCTCCCTGTCTCCGGGTAA 1427	
Y	1466	ATGA 1469	
Ω	1428	AIGA 1431	

APPLICANT: Anderson, Darrell R. TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

Sequence 11, Application US/09948429B Patent No. US20020177689A1 GENERAL INFORMATION:

ESULT 14 S-09-948-429B-11

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TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS" NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 CTTGGGGCTGCTCTTCTGCCTGGTGA¢ATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 GAAGCAGTCAGGACCTGGCCTAGTGCAGGCCTCACAGAGCCTGTCCATCACCTGCACAGT 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 GGGTCTGGAGTGGCTGGGAGTGATAT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9; Length 1431;
                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.7%; Score 630.8; DB 9;
67.6%; Pred. No. 7.9e-185;
Live 0; Mismatches 432;
                                                                       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 012712-131
                                                                                                                                                                                                                                                                                                                                                                                                     US 08/487,550
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 67.6*
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Teskin, Robin L. REGISTRATION NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat_peptide
LOCATION: 1.1431
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                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: APPLICATION NUMBER:
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                                                                                                        Alexandria
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                                                                                                                                              COUNTRY:
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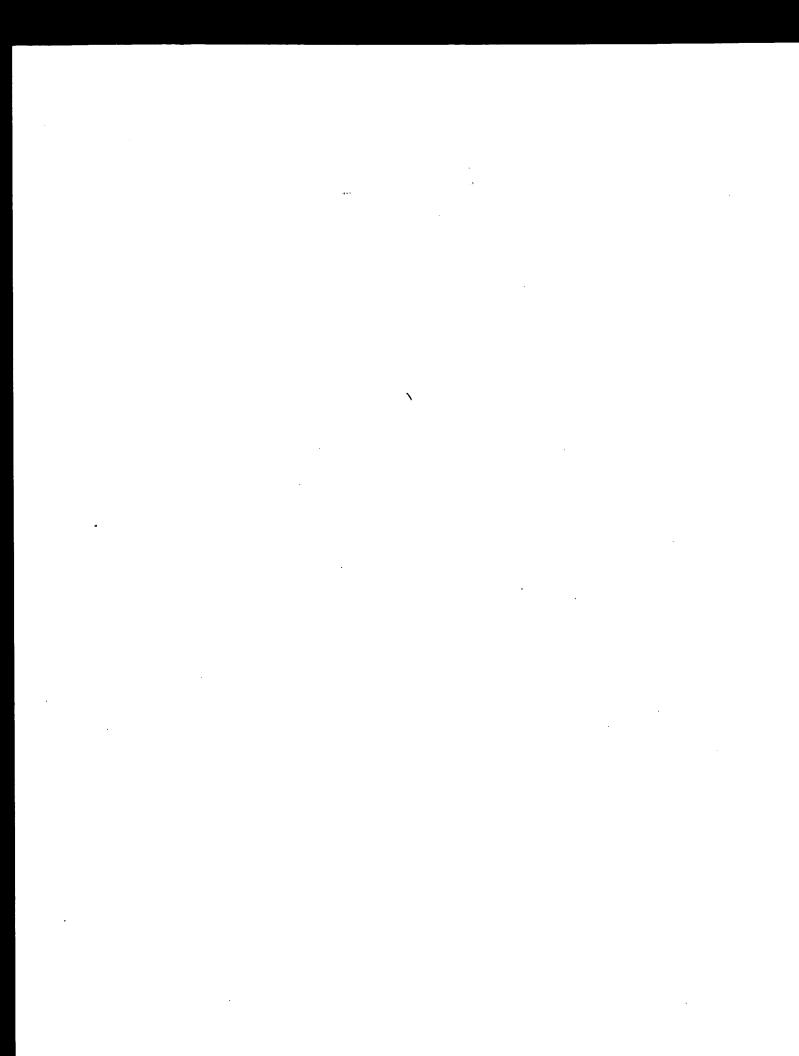
1466 ATGA 1469

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986 TCAGACACAAACCCATAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCTCCC 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         746 ACTTGAGCCCAGGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCA 805
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389 GGATAITIACTAIGAITICACTIAIGCCAIGGACIACIGGGGICAAGGAACCICAGICAC 448
                                                                     369 AGTIGITGGAATGGTITACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTCCTGGTCAC 428
                                                                                                                                                        449 CGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGA 508
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                                                                                                                                                                                                                                                                                                                    509 TACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGT 568
                                                                                                                                                                                                                                                                                                                                                                                                      489 CACCTCTGGGGGCACAGCGGCCCTGGGCTGCTCGAAGGACTACTTCCCCGAACCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 GACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCCACCTTCCCAGCTCTCCT
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TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 CCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCEAGGTGCAGCT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0; Mismatches 433; Indels
                                                                                                                                                                                                                                                                                            AND B7.2 CO-STIMULATORY ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <Unknown>
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                  APPLICANT: ANDERSON, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         Sequence 6, Application US/10073138 Publication No. US20020187146A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                          HANNA, Nabil
BRAMS, Peter
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria
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Sequence 17, Appl
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Sequence 6, Appli
Sequence 19, Appli
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Sequence 23, Appl
Patent No. 5455030
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Sequence 49, Appl
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                         149 GIGAAGAIGTCCTGCAAGGCTTCTGGCTACACCTTTACTAGGTACACGAIGCACTGGGTA 208
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                                                   21 CTCCATCAGAGCATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGT 80
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1098 AACAAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAAAGGGCTAGTCAGA 1157
                      1158 GCTCCACAAGTATACATCTTGCCGCCACCAGCAGGAGCAGTTGTCCAGGAAAGATGTCAGT 1217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Humanised Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/303,569B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08303569B Patent No. 5859205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Athwal, Diljeet S. APPLICANT: Emtage, John S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adair, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1578 AAAAAAA 1585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1556 AAAAAAA 1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-303-569B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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FILING DATE: 03-DEC-1993 נגטט משם 81 GTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGC 140 141 CTGTCCATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGGTATGGTGTACACTGGGTT 200 201 CGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGA---GTGATATGGAGTGGTGGAGAC 257 258 ACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGC 317 494 GTGTGTGGAGATACAACTGGCTCCTCGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTC 553 798 GAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCT 857 318 CAACTCTTCTTTAAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACTGTGCC 377 378 AGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGGTCAAGGA 437 438 ACCTCAGTCACCGTCTCCAGCCAAAACAACCCCCCATCAGTCTATCCACTGGCCCCT 497 GGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTC 557 558 CCTGAGTCAGTGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACCTTC 617 618 CCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGC 677 738 GACAAAAAACTTGAGCCCAGCGGCCCATTTCAACAATCAACCCTGTCCTCCATGCAAG 797 21 CTCCATCAGAGCATGGCTGTCTTGGGGCTGCTTCTTGCCTGGTGACATTCCCAAGCTGT 80 29 CTCTGACTCAACATGGAAAGGCACTGGATCTTTCTACTCCTGTTGTCAGTAACTGCAGGT 88 Query Match

Soure 939.2; DB 2; Length 1570;
Best Local Similarity 77.1%; Pred. No. 9.5e-265;
Matches 1209; Conservative 0; Mismatches 323; Indels 36; Gaps LENGTH: 1570 base pairs TYPE: nucleic acid STRANDEDNESS: single mat_peptide 98..1444 41..1444 MOLECULE TYPE: CDNA linear NAME/KEY: LOCATION: NAME/KEY: TOPOLOGY: LOCATION: S-08-303-569B-6 498 FEATURE

δŏ	828	CCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGGTGGTG 917
QQ	836	CCAAAGATCAAGGATGTACTCATGATCTCCCTGAGCCCCCATAGTCACATGTGTGTG
Qy	918	GATGTGAGCGAGGATGACCCAGACGAGTCAGCTGGTTTGTGAACAACGTGGAAGTA 977
Qy	978	10
qq	926	
Qy	1038	ACCCTCCCCATCCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1097
οp	1016	GCCCTCCCCATCCAGCACCAGGACTGGCAAGGAGGAGTTCAAATGCAAGGTCAAC 1075
Qy	1098	AACAAAGACCICCCAICACCCAICGAAAAACAICTCAAAAAITAAAGGCIAGICAGA 1157
qq	1076	AACAAAGACCTCCCAGCGCCCATCGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGA 1135
Οy	1158	GCTCCACAAGTATACATCTTGCCGCACCAGCAGGAGGCAGTTGTCCAGGAAAGATGTCAGT 1217
qq	1136	GCTCCACAGGTATATGTCTTGCCTCCACCAGAAGAAGAGATGACTAAGAAACAGGTCACT 1195
QY	1218	CTCACTTGCCTGGTCCTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAAT 1277
δλ	_	133
qa	1256	3
Qy	1338	TTCATATATAGCAAGCTCAATATGAAACAAGCAAGTGGGAGAAAACGAATTCCTTCTCA 1397
qq	1316	TICATGTACAGCAAGCTGAGAGGAGAAGAAGAACTGGGGTGGAAAGAAA
δλ	1398	TGCAACGTGAGACACGGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCT 1457
qq	1376	TGTTCAGTGGTCCACGAGGGTCTGCACAATCACCACGACTAAGAGCTTCTCCCGGACT 1435
Qy	1458	CCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCAT 1517
qq	1436	CCGGGTAAATGAGCTCAGCACCCACAAAACTCTCAGGTCCAAAGAGACACCCACACTCAT 1495
Oy,	1518	ATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAAGCCTGGTACCATGTAAAAAAA 1577
qq	1496	CTCCATGCTTCCCTTGTATAAATAAAGCACCCAGCAATGCCTGGGACCATGTAAAAAA 1555
Qy	1578	158
qq	1556	AAAAAAA 1563
RESUUS-OUS-OUS-OUS-OUS-OUS-OUS-OUS-OUS-OUS	SULT 3 -08-353-400- Sequence 23, Patent No. 5 GENERAL INE APPLICANT TITLE OF COMPUTER MEDIUM	ESULT 3 S-08-353-400-23 Sequence 23, Application US/08353400 Patent No. 566357 GENERAL INFORMATION: APPLICANT: TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 37 COMPUTER READABLE FORM: MEDIUM TYPE: Florow disk
	COMPUTE OPERATI SOFTWAR	R: IBM PC compatible NG SYSTEM: PC-DOS/MS-DOS E: PatentIn Release #1.0, Version #1.25 (EPO)
•• ••	CURRENT A APPLICA	4
	CLASSIF PRIOR APP	FILING DAIE: CLASSIFICATION: 424 RIOR APPLICATION DATA:
. *	APPLICA FILING	TION NUMBER: GB 9324819.3 DATE: 03-DEC-1993

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           52 TCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 TGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTCTTAAAATGAACAGTCTGCGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 CTACTGACACACATATATTACTGTGCCAGAAATAGAGGGGGATATTTACTATGATTTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 CTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 ACGATGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCTGCCAAAACGA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 CACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGA 528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 GGGCTGAACTGGTGAAGCCTGGGGGCTTCAGTGCAGCTGCTGCAAGGCTTCTGGCTACA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 CATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 CCTTCACCGGCTACTGGATACACTGGGTGAAGCAGAGGCCTGGACAAGGCCTTGAGTGGA 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 TCCTCTTTTTGGTAGCAACAGGTACAGATGTCCACTCCCAGGTCCAACTGCAGCAGCCTG 127
                                                                                                                                                                                                                                                                                                   45.4%; Score 720.4; DB 1; Length 1572;
69.2%; Pred. No. 8.9e-201;
tive 0; Mismatches 426; Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 779 GTAAGCCTTGCATATG------
                       GB 9411089.7
                                                                        INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) -08-353-400-23
                       APPLICATION NUMBER: GB 9-
FILING DATE: 03-JUN-1994
                                                                                                                          LENGTH: 1572 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            Matches 1065; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                          linear
                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                          Best Local
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1129 CCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAG 1188
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                                                                                                                                                                                                    1009 ATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGA 1068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1309 CACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGCAAGCTCAATATGAAAACAA 1368
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                          863 TGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGT 922
                                                                                                                                            923 TCAGCTGGTTTGTAGATGATGTGGAGGTGCACACACCTCAGACGCAACCCCGGGAGGAGC 982
42.5%; Score 674.4; DB 6; Length 1347; 69.6%; Pred. No. 2.3e-187;
                                                                                                                     APPLICANT: LADNER, ROBERT C.;BIRD, ROBERT E.;HARDMAN, KARL TITLE OF INVENTION: IMMUNOTHERAPHY USING SINGLE CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 512,910
FILING DATE: 25-APR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
FILING DATE: 02-SEP-1987
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Patent No. 5455030
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Matches	962; Conservative 0; Mismatches 381; Indels 39; Gaps 2;
	AGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCGCTCACAGAGCCTGTCCATCA 1
	51 CCTGCACAGTCTCTGTTTTCTCATTAACTAGGTGTACACTGGGTTCGTCAGTCTC 210
7 . 7	211 CAGGAAAGGGTCTGGAGTGGAGTGATATGGAGTGGTGGAGACACAGACTATA 267
	ATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGACATTCCAAGAGCCAACTTTCT
11	
	328 TIAAAATGAACAGTCTGCGAGCTACTGACAGCCATAITACTGTGCCAGAAATAGAG 387
36 36	388 GGGATATTTACTATTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCA 447
.4 .8	448 CGGTCTCCTCAGCCBAAACAACCCCCCATCAGCTCTATCCACTGGCCCCTGGGTGTGGG 507
501	508 ATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGCTACTTCCCTGAGTCAG 567
56	568 TGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACCCTTCCCAGCTCTCC 627
54 62	628 TGCAGTCTGGACTCTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAA 687
9 9	688 GTCAGACCGTCACCTGCAGGGTTGCTCACCCAGCAGCAGCAGCAGGTGGACAAAAAC 747
74	748 TTGAGCCCAGGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACA 807
8 8 6 9	08 AATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAATATCA 867
861	68 AGGATGTACTCATGATCTCCTGACACCCAAGGTCACGTGTGGTGGTGGTGGATGTGAGCG 927 -
8 92	928 AGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAGGGGAAGTACACACAGGTC 987
998	88 AGACACAAAACCCATAGAAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCA 1047 111 11 11 11 11 11 11 11
1048	B TCCAGCACCAGGACTGGATGAGTGGCAAGGACTTCAAATGCAAGGTCAACAACAAAGACC 1107
1108	TCCCATCACCATCGAGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAG 116
<u>,</u>	

1408 GACACGAGGGTCTGAAAATTACTACTTGCAAGAAGACCATCTCCGGGTCTCCGGGGTAAAT 1467 1228 TGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAG 1287 1348 GCAAGCTCAATATGAAAACAAGCAAGHGGGAGAAAACAGATTCCTTCTCATGCAACGTGA 1407 1168 TATACATCTTGCCGCCACCAGCAGAGCTTGTCCAGGAAAGATGTCAGTCTCACTTGCC 1227 APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Vue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Bughn, Mariah R.
APPLICANT: Bughn, Mariah R.
APPLICANT: Bughn, Mariah R. SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/09/049,672A FILING DATE: HEREWITH CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555 Sequence 17, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. 39,132 INFORMATION FOR SEQ ID NO: 17: IBM Compatible NAME: Cerrone, Michael C REGISTRATION NUMBER: 39,1 ATTORNEY/AGENT INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 1567 base pairs TYPE: nucleic acid STRANDEDNESS: single TELEPHONE: 650-855-055 TELEFAX: 650-845-4166 Diskette CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: COMPUTER READABLE FORM: MEDIUM TYPE: Diskett OPERATING SYSTEM: Palo Alto USA 1468 GA 1469 1346 GA 1347 FILING DATE: 94304 CA RESULT 5 US-09-049-672A-17 COMPUTER: COUNTRY: STATE: φ ŏ

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REGISTRATION NUMBER: 24,618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 ATAGAGGGGATATITACIATGATTICACITATGCCATGGACTACIGGGGTCAAGGAACCT 441
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                                                                                                                                                                                                                                                                                                                                                                                              88 CCCAGGIGCAGCIGAAGCAGICAGGACCIGGCCIAGIGCAGCCCICACAGAGCCIGICCA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 CCCAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 TCACCTGCACAGTCTCTGGTTTCTCATTAACTAGGTATGGTGTACA-----CTGGGTTC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 TCACCTGCGCTGTCTCTGGTGGCTCCATCACTAGTGGTGGTTACTACTGGAGCTGGATCC 252
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                                                                                                                                                                                                                                                                                   28 AGAGCATGGCTGTTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTAT 87
                                                                                                                                                               41.0%; Score 651.8; DB 3; Length 1567;
67.4%; Pred. No. 1e-180;
tive 0; Mismatches 447; Indels 33; Gaps
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                                                         LIBRARY: PANCTUT01
CLONE: 1513264
                                                                                                                                                                                                    Similarity
TOPOLOGY: linear
                            IMMEDIATE SOURCE:
                                                                                                              -09-049-672A-17
                                                                                                                                                                       Query Match
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1189 AACCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCC 1248
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                                             1009 ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCG 1068
                                                                                          1039 CCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACA 1098
                                                                                                                                                                                       1099 ACAAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAG 1158
                                                                                                                                                                                                                                    1129 ACAAAGCCCTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAG 1188
                                                                                                                                                                                                                                                                               1159 CTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTC 1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/08793450 Patent No. 6312690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARGARITIE, CHRISTEL
KACZOREK, MICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: EDELMAN, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Db 680 TGAATCAAGCCCAGCAACACCAAGGTGGACAAGAAAGCACACACA	829	Qy 889 TGACACCCAAGGTCACGTGTGTGGTGGTGGAGTGAGCGAGG	QY 949 TCAGCTGGTTTGTGAACAAGGTGGAAGTACACAGGTCAG.	Qy 1009 ATTACAACAGTACTATCCGGGTGGTCAGCCCTCCCCATC 	Qy 1069 GTGGCAAGGAGTTCAAATGCAAGGT¢AACAACAAAGACCTCC	Qy 1129 CCATCTCAAAATTAAAGGGCTAGTGAGGCTCCACAAGTA:	QY 1189 CAGAGCAGTTGTCCAGGAAAGATGT¢AGTCTCACTTGCCTGC	QY 1249 GAGACATCAGTGTGGAGTGGACCAGGAATGGGCATACAGAGC	Qy 1309 CACCAGICCIGGACICTGACGGIICTTACIICAIAIAIAGC)	OY 1369 GCAAGTGGGAGAAAACAGATTCCTTGTCATGCAACGTGAGAC	Oy 1429 ACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATG 1	RESULT 7 US-08-467-420A-49 ; Sequence 49, Application US/08467420A	; Patent No. 5683892 ; GENERAL INFORMATION: ; APPLICANT: Ames, Robert S. ; APPLICANT: Appelbaum, Edward R.	; APPLICANT: Chalken, Irwin M. ; APPLICANT: Cook, Richard M. ; APPLICANT: Gross, Mitchell S. ; APPLICANT: Holmes, Stephen D.	; APPLICANT: MCMillan, Lynette J. ; APPLICANT: Theisen, Timchiw W. ; TILLE OF INVENTION: Treatment of IL5 Antagonists Us ; TITLE OF INVENTION: Treatment of IL5 Mediated Disc	CORRESPONDENCES: /4 CORRESPONDENCE ADDRESS: ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property	; STREET: P. O. Box 1539-UW2220 ; CITY: King of Prussia
回路無数の可用	TYPE: nu STRANDEDN TOPOLOGY: MOLECULE TY	FEATURE: NAME/KEY: CDS LOCATION: 1.1418 FEATURE	; NAME/KEY: sig_peptide ; LOCATION: 157 ; FEATURE:	NAME AND SECONDARY SECONDARY SECONDARY SECONDARY STREET INFORMATION: /product= "IMMUNOGLOBIN, HEAVY CTHER INFORMATION: CHAIN" GRAIN"	Query Match 41.0%; Score 651.2; DB 4; Length 1418; Best Local Similarity 67.5%; Pred. No. 1.4e-180; Matches 958; Conservative 0; Mismatches 438; Indels 24; Gaps 2;	ANTICCCAAGCTGTGTCCTATCCCAGGTGCAGGTGAAGCAGTCAG 11						2Y 412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAAAAAA	2y 472 CCCCATCAGTCTATCCACTGGGTGTGGAGATACAACTGGTTCCTCGTGACTC 531	2Y 532 TGGGATGCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGAT 591 1111	3y 592 CCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTGCAGTCTGGACTCTACACTA 648	2Y 649 TGACCAGCTCAGTGACTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCGG 708	3y 709 tigetcacccagccagcaccacggtggacaaaaacttgagcccagcgggcccatt 768

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ACACGGGGTCTGAAAATT 1428
                                                                              GACACAAACCCATAGAGAGG 1008
                                                                                                    CCAGCACCAGGACTGGATGA 1068
                                                                                                                                                    ATACATCTTGCCGCCACCAG 1188
                                    AGGATGTACTCATGATCTCCC 888
                                                                                     SGTGCCCAGCACCTGAACTCC 778
                                                               GGATGACCCAGACGTCCAGA 948
               ATGCCCAGCTCCTAACCTCG 828
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1598 CAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGC 1657
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APPLICANT: Holmes, Stephen D.
APPLICANT: McMillan, Lynette J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ames, Robert S.
APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
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                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 40.1%; Score 637.4; DB 1; Local Similarity 68.2%; Pred. No. 3.3e-176; les 947; Conservative 0; Mismatches 406;
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                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      PC-DOS/MS-DOS
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
                                                                                                                                                                                                                                                                                                                                                      NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P5(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49:
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LENGTH: 6285 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
        Pennsylvania
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                                                                                                                                  OPERATING SYSTEM:
                                                19406-0939
                            USA
                                                                                                                                                                                                                             FILING DATE:
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                            COUNTRY:
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1407 AGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAA 1466
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                                                                    1658 ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA 1717
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687 AGTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAA 746
                                                                                                                                           747 CTTGAGCCCAGCGGGCCCATTTCAACAATCAACCCTGTCCTCCATGCAAGGAGTGTCAC 806
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1538 ACGGTGTGGAACTCAGGCGCCCTGACCAGCGCGCGTGCACCTTCCCGGCTGTCCTA 1597
                                                                                                                                 1658 ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACAAGGTGGACAAAGAGA 1717
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                      570 ACTGIGACTIGGAACTCIGGAICCC#GICCAGCAGIGIGCACACCTICCCAGCICICCIG 629
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; Patent No. 5783184
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Appelbaum, Edward R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 GTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCTGGGTGTGGAGAT 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 ACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTG 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.1%; Score 637.4; DB 1; Length 6285; 68.2%; Pred. No. 3.3e-176;
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TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
             NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corp./Corporate
ADDRESSEE: Intellectual Property
STREET: P. O. Box 1539-UW2220
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/470,110A
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/363131
FILING DATE: 23-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6285 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 610 270-5090 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Matches 947; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: double
                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                 Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
                                                                                                                                                                                       19406-0939
                                                                                                                                                                     USA
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                                                                                                                                                                                                                                      MEDIUM TYPE:
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                                                                                                                                                                 COUNTRY:
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                                                                                                                                               STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            270 GCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 CAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 ACCTGCACAGTCTCTGGTTTCTCATTAACTAGGTGTTGGTGTACACTGGGTTCGTCAGTCT 209
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                                                                                                               TITLE OF INVENTION: Recombinant LL5 Antagonists Useful in TITLE OF INVENTION: Treatment of LL5 Mediated Disorders
                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                        SmithKline Beecham Corp./Corporate P.O. Box 1539-UW2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US95/17082
FILING DATE: 22-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/667,769A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 08/470110
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                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P50503
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
                                                                           McMillan, Lynette J.
Theisen, Timothy W.
                                      Gross, Mitchell S.
Holmes, Stephen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
 Chaiken, Irwin M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49
                     Cook, Richard M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-1994
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                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6285 base pairs
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                                                                                                                                                                                                                         King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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EDNESS: double
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                                                                                                                                                                                                                                            Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 06-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                   19406-0939
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                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                            ADDRESSEE:
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APPLICANT:
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1107 CICCCAICACCCATCGAGAGAACCAICICAAAAAITAAAGGGCTAGICAGAGCTCCACAA 1166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1817 AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGC 1876
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                                                                                                                                                                                                                                                                                                             1658 ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGA 1717
                                                               1310 ACCATGACTAACATGGACCCGGTTGACACCGCTACCTACTACTGCGCTCGAGA----- 1362
                                                                                                                                                                       1363 ----TCCCCCTTCTTCCTTACTACGCCTTGACTACTGGGGTCGTGGTACCCCAGTTACT 1417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1538 ACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTA 1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          570 ACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTG 629
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330 AAAATGAACAGTCTGCGAGCTACTGACACACCATATATTACTGTGCCAGAAATAGAGGG 389
                                                                                                                                  390 GATATITACTATGATITCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACC 449
                                                                                                                                                                                                                                                                     450 GICICCICAGCCAAAACAACACCCCCAICAGICIAICCACIGGCCCCTGGGIGIGGAGAI 509
                                                                                                                                                                                                                                                                                                                                                                                                     510 ACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTG 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                630 CAG---TCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCA 686
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QY 210 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGAGACACACAC	270	Db 1250 TCGGCTCTCATGTCCCGTTATCCAAAGACTCCCGTAACAAGTTGTTCTG 1309 Ov 330 Abbarcabacacacacacacacacacacacacacacacaca	1310	QY 390 GATATTACTATGACTTATGC CATGGACTACTGGGGTCAAGGAACCTCAGTCACC 449	QY 450 GTCTCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGAT 509 1 1 1 1 1 1 1 1 1	QY 510 ACAACTGGTTCCTCCGTGACTCTGGGTCAAGGGCTACTTCCCTGAGTCAGG 569	Oy 570 ACTGTGAACTCTGGATCCCTGTCCAGCAGTGCGCACCTTCCCAGCTCTCTG 629	Qy 630 CAGTCTGGACTCTACACTATGAGCACCTCAGTGACTGCCCTCCAGCACCTGGCCA 686	QY 687 AGTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCAGCACCACGGTGGACAAAAAA 746	QY 747 CTTGAGCCCAGGGGCCCATTCAACAACCCTGTCCTCCATGCAAGAGTGTCAC 806	QY 807 AAATGCCCAGGTCCTAACCTCGAGGGTGGACCATCGGTCTTCATCTTCCCTCCAAATATC 866	Qy 867 AAGGATGTACTCATGATCTCCCTGACACCTCACGTGTGTGT	Qy 927 GAGGATGACCCCAGATCAGGTGGGTTTGTGAACAACGTGGAAGTACACAGCT 986	QY 987 CAGACACAAACCCATAGAGAGGATTAÇAACAGTACTGGGGGGGGTGGTCAGCACCCTCCCC 1046	OY 1047 ATCCAGCACCAGGACTGGATGAGTGGGTTCAAATGCAAGGTCAACAAGGC 1106 1997 GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGGTCAAGAAGGC 2056	Qy 1107 CTCCCATCACCATGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAA 1166 	QY 1167 GTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAGATGTCAGTCTCACTTGC 1226 DD 1	Qy 1227 CTGGTGGGCTTCAACCCTGGAGAQATCAGTGGAGTGGACCAGCAATGGGCATACA 1286
	2417 TGAGTGTAG 242	RESULT 10 15-08-940-371-49	Sequence 49, Application US/08940371 Patent No. 5851525 GENERAL INFORMATION:	APPLICANT: Ames, Robert S. APPLICANT: Appelbaum, Edward R. APPLICANT: Chalken, Irwin M. APPLICANT: Cook Richard M		TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in TITLE OF INVENTION: Treatment of IL5 Mediated Disorders NUMBER OF SEQUENCES: 74 CORRESPONDENCE ADDRESS:	ADDRESSEE: SmithKline Beecham Corp./Corporate ADDRESSEE: Intellectual Property STREET: P. O. Box 1539-UW2220 CITY: King of Prussia	STATE: Pennsylvania COUNTRY: USA ZIP: 19406-0939 COMPITER READARIE FORM:	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ParentTn Release #1 0 Vorsion #1 25	A: US/08/940,371	PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/470,110 FILING DATA: APPLICATION NUMBER: US/08/353131	C-199 ATION rey A	REFERENCE/DOCKET NUMBER: P50282 TELECOMMUNICATION INFORMATION: TELEPHONE: 610 270-5024 TELEFEX: 610 270-5090	INFORMATION FOR SECTION OF SECTIO	. 무직적단	Query Match 40.1%; Score 637.4; DB 2; Length 6285; Best Local Similarity 68.2%; Pred. No. 3.3e-176; Matches 947; Conservative 0; Mismatches 406; Indels 36; Gaps 3;	Y 90 CAGGIGCAGCIGAAGCAGICAGGACCIGGCCIAGIGCGCICACAGAGCCIGICCAIC 149	150 ACCTGCACAGTCTCTCATTAACTAGGTGTACACTGGGTTCGTCAGTT 209

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1167 GTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGC 1226
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                               2237 GAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT 2296
                                                                  1347 AGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTG 1406
                                                                                                                                    1407 AGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAA 1466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Recombinant 1L5 Antagonists Useful i
TITLE OF INVENTION: Treatment of 1L5 Mediated Disorders
NUMBER OF SEQUENCES: 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: SmithKline Beecham Corp./Corporate
SSEE: Intellectual Property
P. P. O. Box 1539-UW2220
King of Prussia
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19-30N-1997
18: 536
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                                                                                                                                                                                                                                                                                                                         Sequence 49, Application US/08637647 Patent No. 6129913
                                                                                                                                                                                                                                                                                                                                                                                                                                Cook, Richard M.
Gross, Mitchell S.
McMillan, Lynette J.
Theisen, Timothy W.
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APPLICANT: Appelbaum, Edward R.
APPLICANT: Chaiken, Irwin M.
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Best Local Similarity 68.2%
Matches 947; Conservative
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1107 CTCCCATCACCCATCGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAA 1166 1817 AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGC 1876 1937 AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACC 1996 1363 -----recectretretretreGGCTTGACTACTGGGGTCGTGGTACCCCAGTTACC 1417 1658 ACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCCAAGGTGGACAAGAA 1717 1718 GTTGAGCC------CAAATCTTGTGACAAAACTCACACACATGCCCA 1756 987 CAGACACAAACCCATAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCC 1046 1130 ACCTGCACCGTCTCCCGTTTCTCCCTGACGACTATAGTGTACACTGGGTCCGTCAGCCG 1189 1190 CCGGGTAAAGGTCTAGAATGGCTGGGTGTAATATGGGCTAGTGGAGGCACAGATTATAAT 1249 1310 ACCATGACTAACATGGACCCGGTTGACACCGCTACTACTGCGCTCGAGA----- 1362 1418 GIGAGCICAGCIAGIACCAAGGGCCCATCGGICITCCCCCTGGCACCCTCCTCCAAGAGC 1477 1478 ACCTCTGGGGGCACAGCGGCCTGGTGGTGACTACTTCCCCGAACCGGTG 1537 1070 CAGGITACCCIGCGIGAATCCGGICCGGCACTAGTTAAACCGACCCAGACCTGACGTTA 1129 867 AAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGTGTGAGC 926 927 GAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCT 986 747 CTTGAGCCCAGCGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCAC 806 807 AAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATC 866 270 GCAGCTITCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTT 329 330 AAAATGAACAGTCTGCGAGCTACTGACACCCATATATTACTGTGCCAGAAATAGAGGG 389 390 GATAITIACTATGATITICACITATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACC 449 450 GTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGAT 509 510 ACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTG 569 570 ACTGTGAACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACCACCTTCCCAGCTCTCCTG 629 630 CAG---TCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCA 686 687 AGTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCAGCACCACGGTGGACAAAAA 746 210 CCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGGTGGAGACACACAGACTATAAT 269 150 ACCTGCACAGTCTCTGGTTTCTCATTAACTAGGTGTAGTGTACACTGGGTTCGTCAGTCT 209 90 CAGGIGCAGCIGAAGCAGICAGGACCIGGCCIAGIGCAGCCCICACAĞAGCCIGICCAIC 149

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	CTGGTCGTGGGCTTCAACCCTGGAGCATCAGTGGAGTGG	1287 GAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATAT 1346 	1347 AGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTG 1406 	1407 AGACACGAGGGTCTGAAAAATTACTACCTGAAGAAGACGATCTCCGGGTGTCGGGTAAA 1466 		TESULT 12 CT-USSS-17082A-49 CENERAL INFORMATION GENERAL INFORMATION GENERAL INFORMATION APPLICANT: Appelbaum. Edward R. APPLICANT: Appelbaum. Edward R. APPLICANT: GOOK, RICHARD M. APPLICANT: GOOK, RICHARD M. APPLICANT: GOOSS, MITCHELD J. APPLICANT: Holmes, Scephen D. APPLICANT: Holmes, Scephen D. APPLICANT: Holmes, Scephen D. APPLICANT: MANIAL Infootly M. APPLICANT: Holmes, Scephen D. APPLICANT: MANIAL M. APPLICANT: MANIAL M. APPLICANT: MANIAL M. COUNTRY: USE STALKHILINE Beecham Corp./Corporate STREET: P. O. Box 1339-UW2220 STREET: P. O. Box 1339-UW2220 STREET: P. O. Box 1339-UW2220 STREET: P. O. Dox 1339-UW2220 STREET: P. O. Dox 1339-UW2220 CONTRY: WISE COMPABLE FORM: WEDDIN TYPE: Floppy disk COMPUTER: INP PC COMPABLE FORM: WEDDIN TYPE: Floppy disk COMPUTER: INP PC COMPABLE FORM: WEDDIN TYPE: GOORGE FORM: WEDDIN TYPE: GOORGE FORM: WEDDIN TYPE: GOORGE FORM: PRICE APPLICATION NUMBER: US 08/470110 PRICE APPLICATION DATE: PRICE APPLICATION NUMBER: US 08/470110 PRICE APPLICATION NUMBER: US 08/47010 PRICE APPLICATION NUMBER: US 08/47010 PRICE APPLICATION NUMBER: US 08/47010 PRICE APPLICATION NUMBER: 13/028 RESERVEDANCE NUMBER: 13/028 RESERVEDANCE NUMBER: 13/029 TELECOMMULICATION NUMBER: 13/030 TELECOMMULICAT
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1363 -----TCCCCCTTCTTCCTTACGCTTGACTACTGGGGTCGTGGTACCCCAGTTACC 1417
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                                                 TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
LENGTH: 6285 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 68.29
Matches 947; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2297 AGCAAGCTCACCGTGGACAAGAGCAGGGGGGGACGTCTTCTCATGCTCGTG 2356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1937 AAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCTCACC 1996
                                    1047 ATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGAC 1106
                                                                                                                                                       2057 CTCCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG 2116
                                                                                                                                                                                                1167 GTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGC 1226
                                                                                                                                                                                                                                     2117 GTGTACACCCTGCCCCCATCCCGGGAGGAGGATGACCAAGAACCAGGTCAGCCTGACCTGC 2176
                                                                                                                                                                                                                                                                              1287 GAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGTTCTTACTTCATATT 1346
                                                                                                                                                                                                                                                                                                                                                                                                   2237 GAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTAT 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                        1347 AGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTG 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1407 AGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAA 1466
                                                                           1997 GTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCC 2056
                                                                                                                    1107 CTCCCATCACCCATCGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAA 1166
                                                         APPLICANT: BRAMS, Peter
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: CHAMAT, Soulaima Salim
APPLICANT: MALSH BARD
APPLICANT: WALSH BARD
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MEUTRALIZING HIBDLES SPECIFIC TO
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burns, Doane, Swecker & Mathis
                                                                                                                                           APPLICATION NUMBER: US/08/488,376 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08488376
Patent No. 5811524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (703) 836-66
TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R: P.O. Box 1404
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1467 TGAGCTCAG 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2417 TGAGTGTAG 2425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -08-488-376-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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383 ACCTATACTACCTGGATTATTGGGGGCAGGGAACCCTGGTCACCGTCTCCTCAGCTAGCA 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  643 ACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   703 GCAGCGTTGCTCACCCAGCCAGCACCACGACGTGGACAAAAAACTTGAGCCCAGCGGGC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        763 CCATITICAACAATCAACCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTA 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            735 ------CAAATCTTGTGACAAAACTCACACGTGCCCAGCGTGCCCAGCACCTG 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         823 ACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             782 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTCATGA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883 TCTCCCTGACACCCAAGGTCACGTGTGTGGTGGATGTGAGCGAGGATGACCCAGACG 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 TCAGCAACCCTAGAATGGGTGTGACCTGGATCCGTCAGCCCCCGGGAAGGCCCTAGAAT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 GCCTGGGAGTGATATGGAGTGGTGGAGACACACACTATAATGCAGCTTTCATATCCAGAC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 IGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTCTGCGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 TCACCACCTCCCAGACACCTCCAGAAGCCAGGTGGTCCTAAGCTTGACCAACGTGGACC 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349 CTACTGACACACCATATATTACTGTGCCCAGAAATAGAGGG----GATATTACTATGATT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 CTGTGGACACACCACATATTACTGTGCACGGGTAGGACTGTATGACATCAATGCTTATT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 TCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               466 CAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCG 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 CCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           683 GCAACGTGAATCACAAGCCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGCC----- 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 TAA-----CTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 GGCTTGGAAACATTTTTCGAGTGACGAGAAGTCCTTCAGTCCTTCTCTGAAGAGCAGAC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 CTGGCCTAGTGCCAGCCCTCACAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 TCTTCCTTGTCGCTGTTGCTACGCGTGTCCTGTCCCAGGTGCAGTGCAGGAGTCTGGTC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 TGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 586 CTGGATCCCTGTCCAGCAGTGTGCACCTTCCCAGCTCTCCTGCAG---TCTGGACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              623 ACTCCCTCAGCAGCGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Score 634.6; DB 1; Length 1428; 67.6%; Pred. No. 1e-175; tive 0; Mismatches 429; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 965; Conservative
                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        1..1428
                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     est Local Similarity
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Db 842		; , AT	FILING ATTORNEY/
Qy 943 Db 902	3 TCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACAGCGCTCAGACACAAACCCATA 1002 	H	NAME: REGISTRA REFERENT TELECOMMUI
Qy 1003 Db 962	GAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACT 1062 	; INFO	TELEPHOI TELEFAX INFORMATION SEQUENCE (
Qy 1063 Db 1022	9 GGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAGACCTCCCATCACCCATCG 1122 		LENGTH: TYPE: I STRANDEI TOPOLOGY
Qy 1123 Db 1082) AGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGC 1182 		MOLECULE : FEATURE: NAME/KE! LOCATIO!
2y 1183 5b 1142	CACCAGCAGAGCAGTTGTCCAGAAAGATGTCAGTTGCCTGGTCGTGGGGCTTCA 1242 	US-08-6 Query Best	cia i
2y 1243	ACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAACTACAAGG 1302	Matches Qy	es 965;
	ACACCGCACCACCACCACCACCACCACCACCACACACAC	qq	23
		Qy	115 (
2y 1363	AAACAAGCAAGTGGGAGAAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGA	qa	83 (
ob 1322	ACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCGTGATGCATGAGGCTCTGC 1381	λ t	175
2y 1423	AAAATTACTACCTGAAGAAGACCATCTCCGGGTCTCCGGGTAAATGA 1469	g :	143
Jb 1382	ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1428	ζ. Dp	203
RESULT 14 1S-08-634-223-12		Qy	289
Sequence 17	Sequent 2.7, Application US/08634223 Patent No. 5840298	qq	263
GENERAL INF	GENERAL INFORMATION: APPLICANT: HRAMS. Peter	Qy	349 (
APPLICANT:	CHAMAT,	QQ	323 (
APPLICANT:	WALSH,	QY	406 1
APPLICANT:	Ž	QQ	383 1
TITLE OF	TITLE OF INVENTION: MEDITALIZANG ANTIBODIES SPECIFICAR REVENUE AND TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFICARY OF THE TOP TO THE THE WEBSTAND THE WEBST	Qγ	466
NUMBER O	ATTIONS FOR THEIR MANUFACTORE AND INERAFECTION OF 1 19	qa	443 0
ADDRESSEE:	SEE: Burns Donne, Swecker & Mathis	δλ	526 T
CITY:	Alexandria	QΩ	503 C
COUNTRY:	** ()	Qy	286 0
COMPUTER	COMPUTER READABLE FORM: MEDITIM TYPE: Flored disk	qq	563
COMPUTER: OPERATING	IBN	Qy	643 P
SOFTWARE:		qa .	623 A
APPLICATION FILING DATE	APPLICATION NUMBER: US/08/634,223	Qy	703

FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/488,376

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TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCCTAGTGCAGCCCTCACAGAG¢CTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IAA-----CTAGCTATGGTGTACAQTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTGGGAGTGATATGGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGAC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTTGGAAACATTTTTTCGAGTGAGGAGAGTCCTTCAGTCCTTCTCTGAAGAGCAGAC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAGCATCAGCAAGGACAATTCCAAQAGCCAACTCTTTTAAAATGAACAGTCTGCGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTACTGACACAGCCATATATTACTGTGCCAGAAATAGAGGG---GATATTTACTATGATT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCACTTATGCCATGGACTACTGGGGIJCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAA 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCTATACTACTGGATATTGGGGGCAGGGAACCCTGGTCACCTCCTCCTCAGCTAGCA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCG 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           703 GCAGCGTTGCTCACCCAGCCAGCAGCACGTGGACAAAAAAACTTGAGCCCAGCGGGC 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACACTATGAGCAGCTCAGTGACTGTCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            763 CCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCCAGCTCCTA 822
                                                                                                                                                                                                                                                                                                                                                                                                                 40.0%; Score 634.6; DB 2; Length 1428; Similarity 67.6%; Pred. No. 1e-175; Conservative 0; Mismatches 429; Indels 33; Gaps
                                                                                 012712+150
                                                                                                                   HONE: (703) 836-6620

AX: (703) 836-2021

CON FOR SEQ ID NO: 17:

TE CHARACTERISTICS:
                                      Teskin, Robin L.
RATION NUMBER: 35,030
:NCE/DOCKET NUMBER: 012
UNICATION INFORMATION:
                                                                                                                                                                                                                                                                                           TYPE: DNA (genomic)
                 'AGENT INFORMATION:
07-JUN-1995
                                                                                                                                                                                                            1428 base pairs
                                                                                                                                                                                                                             nucleic acid
DNESS: single
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[ON: 1..1428
3-17
                                                                                                                                                                                                                                                                        linear
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DATE:
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NAME/KEY:
LOCATION:
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                                                                                                                                                                   883 TCTCCCTGACACCCAAGGTCACGTGTGTGGTGGATGTGAGCGAGGATGACCCAGACG 942
823 ACCTCGAGGGTGGACCATCCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGA 882
                                                                                                 782 AACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCTCATGA 841
                                                                                                                                                                                                                                                                    902 TCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGG 961
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HEARD, Cheryl Janne
NEWMAN, Roland Anthony
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CHAMAT, Soulaima Salim
PAN, Li-Zhen
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Patent No. 5866125
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TITLE OF INVENTION:
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406 TCACITATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAA 465
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40.0%; Score 634.6; DB 2; Length 1428;
Best Local Similarity 67.6%; Pred. No. 1e-175;
Matches 965; Conservative 0; Mismatches 429; Indels 33;
                 Patentin Release #1.0, Version #1.30
                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/488,376
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                               APPLICATION NUMBER: US/08/634,224
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                               35,030
                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                             CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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  OPERATING SYSTEM:
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                                                                                                                FILING DATE
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Db	623 ACTCCCTCAGCAGCGFGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCT 682
οy	703 GCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAACTTGAGCCCAGCGGGC 762
Dβ	683 GCAACGTGAATCACAAGGCCCAGCAACACGAGGACAAGAAAGCAGAAGCAGAAGCAGAAGCAGAAGA
Qγ	763 CCATTICAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTA 822
qa	735CAAATCTTGTGACAAACTCACACACGTGCCCACCGTGCCCACCTG 781

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Search completed: June 24, 2003, 01:22:31 Job time : 99.1325 secs

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Monoclonal antibod
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8990.482 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseg/genesegn-embl/NA1989.DAT:*
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Murine pCB223 codi Bicistronic idioty MAA 55.1 heavy cha mRNA encoding gamm Combined cDNA inse Anti-tobacco mosai Sequence encoding Murine anti-BGH MA IAS MBP 90-101 CH1 MBP 1-14 CH1.H.CH2 Heavy chain of anti-BGH MORD TO	T.S.	chain-6His coding sequence. G10; phosphotyrosine; cancer; ers heavy chain-hexahistidine" does not include a start codon" C.
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404 ATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAG 463
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                                                                                                                                                                                                     Novel recombinant monoclonal antibody with 4010-hybridoma type specificity useful in diagnostic procedures, especially for detection of phosphotyrosine-containing proteins in a sample .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specificity. The 3' region of the coding sequence comprises a sequence encoding a histidine tag, and was introduced into the 4G10 heavy chain cDNA by site-directed mutagenesis using the oligonuclectide given in ABL56973. The amended heavy chain cDNA was cloned into a eukaryotic vector and, with a vector for the 4G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinases, for affinity purification of phosphotyrosine proteins and for determining the tyrosine phosphorylation status of one or multiple proteins in a given cell or tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biological/medical research, in diagnosis of a variety of diseases including cancers, to identify cellular substrates for tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     light chain, was used to produce a tagged, secreted, functional recombinant monoclonal antibody in transfected mammalian cells. The recombinant antibody is useful for detecting the presence of phosphotyrosine-containing proteins in a sample, for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the coding sequence for the heavy chain of a recombinant monoclonal antibody having 4G10 hybridoma-type
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Jelinek T;
        Lamarche A,
                                                                                                                                                                                                                                                                                                                                                                                                      Example; Page 54; 60pp; English.
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Matches 1218; Conservative
        Esinger D, Stiles L,
                                                                                         WPI; 2002-393728/42.
                                                                                                                                  P-PSDB; ABB76126
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1304 GACACGAGGGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAAG 1363
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1048 TCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACC 1107
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                                                                                                                                                                                     868 AGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGATGTGAGCG 927
                                                                                                                                                                                                                                                    748 TTGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACA 807
                                                                                                                                                                    808 AATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCA 867
524 TGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAA 583
                                688 GICAGACCGICACCIGCAGCGIIGCICACCCAGCCAGCAGCACCACGGIGGACAAAAAAC 747
                                                                                                                                                                                                                                                                                                        928 AGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACAGAGCTC
                                                                                                                      Monoclonal antibody; antibody; 4G10; phosphotyrosine; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant 4G10 antibody heavy chain coding sequence.
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Unidentified.

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Novel recombinant monoclonal antibody with 4G10-hybridoma type specificity useful in diagnostic procedures, especially for detection of phosphotyrosine-containing proteins in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the coding sequence for the heavy chain of a recombinant monoclonal antibody having 4G10 hybridoma-type specificity. It was obtained by PCR amplification of 4G10 hybridoma cDNA using a 5' primer (see ABL56699) based on the N-terminal sequence of the heavy chain and a 3' primer (see ABL56970) based on prior knowledge of the 4G10 monoclonal antibody. The heavy chain cDNA was cloned into a eukaryotic vector and, with a vector for the 4G10 light chain, was used to produce a secreted, functional recombinant monoclonal antibody in transfected mammalian cells. The recombinant antibody is useful for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            presence of phosphotyrosine-containing proteins in a sample, for use in biological/medical research, in diagnosis of a variety of diseases including cancers, to identify cellular substrates for tyrosine kinases, for affinity purification of phosphotyrosine proteins and for determining the tyrosine phosphorylation status of
                                                                                                                /note= "The CDS does not include a start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                one or multiple proteins in a given cell or tissue sample.
                                                                         /product= "4G10 heavy chain'
                                                                                                                                                                                                                                                                                                                                                            Jelinek
                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Esinger D, Stiles L, Lamarche A,
                                                                                                                                                                                                                                                                                                                   (UPST-) UPSTATE BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 53; 60pp; English.
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DB 24; Length 1365; Score 1081.2; DB 24; Lengtl Pred. No. 1.5e-255; 1; Mismatches 149; Indels 68.1%; 87.6%; Matches 1211; Conservative Local Similarity Query Match

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Sequence 1365 BP; 363 A; 385 C; 331 G; 285 T; 1 other;

GA 1469

1468

388 GGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCA 447

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988 AGACACAAAACCCATAGAGAGGATTAQAACAGTACTATCCGGGTGGTCAGCACCCTCCCCA 1047 1048 TCCAGCACCAGGACTGGATGAGTGGGAAGGAGTTCAAATGCAAGGTCAACAACAAAGACC 1107 1108 TCCCATCACCCATCGAGAGAACCATGTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAG 1167 1004 TCCCATCACCCATGGAGAACCATGTCAAAAATTAAAGGGCTAGTCAGAGGCTCCACAAG 1063 1168 TATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCC 1227 TGGTCGTGGGCTTCAACCCTGGAGAGATCAGTGGGAGTGGACCAGCAATGGGCATACAG 1287 1288 AGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATA 1347 1184 AGGAGAACTACAAGGACACCGCACCAGTCCTGGACGGTTCTTACTTCATATA 1243 GCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGA 1407 1244 GCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGA 1303 403 583 747 643 823 987 507 567 463 627 687 807 644 TIGAGCCCAGGGGCCCATITCAACAATCAACCCCIGTCCTCCATGCAAGGAGTGTCACA 703 867 704 AATGCCCAGCTCCTAACCTCGAGGG#GGACCATCCGTCTTCATCTTCCCTCCAAATATCA 763 927 448 CCGTCTCCTCAGCCAAAACAACACC¢CCATCAGTCTATCCACTGGCCCCTGGGTGTGGGG ATACAACTGGTTCCTCCGTGACTCT¢GGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAG TGACTGTGACTTGGAACTCTGGATC¢CTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCC 464 TGACTGTGACTTGGAACTCTGGATC¢CTGTCCAGCAGTGTGCACCTTCCCAGCTCTCC 628 TGCAGTCTGGACTCTACACTATGAGGAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAA 524 IGCAGICIGGACICIACACIAIGAGGAGCICAGIGACIGICCCCICCAGCACCIGGCCAA 688 GTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCAGCACCACCACGCTGGACAAAAAAC 808 AATGCCCAGCTCCTAACCTCGAGGG#GGACCATCCGTCTTCATCTTCCTCCTCCAAATATCA 928 AGGATGACCCAGACGTCCAGATCAGGTGGTTTGTGAACAACGTGGAAGTACACACAGCTC 302 GGG-----508 268 δ qq δ QQ δy qq δ a δy g δy qq δλ g q pp ρp g å ò δ δy ŏ g ò ŏ В ΩŽ g ŏλ g QQ δy

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1104 GACCTCCCATCACCCATCGAGAGAACCATCTCAAAATTAAAGGGCTAGTCAGAGTCCA 1163
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                                                                                          324 ITCTTTAAAATGAACAGTCTGCGAGCTACTGACACCCATATATTACTGTGCCAGAAAT 383
                                                                                                                                                                                        384 AGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCA 443
                                                                                                                                                                                                                                   427 -----ATCGACTACTACGGAGGGGGGGTTTGGTTACTGGGGCCAAGGGACTCTG 477
                                                                                                                                                                                                                                                                                444 GTCACCGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGT 503
                                                                                                                                                                                                                                                                                                          504 GGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAG 563
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264 TATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTC 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 60.6%; Score 963; DB 15; Length 1645; Best Local Similarity 77.6%; Pred. No. 1.6e-226; Matches 1215; Conservative 0; Mismatches 320; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                               Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region; transform; myeloma cell; light chain; tumour; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences (AAQ54651-52) show the light and heavy chain cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New chimaeric T84.12 antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also DNA encoding it and transformed myeloma cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of murine T84.12. The T84.12 antibody is directed against the tumour marker carcinoma embryonic antigen, and is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1645 BP; 453 A; 444 C; 399 G; 349 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= T84.12_heavy_chain
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                                                                                                                            AAQ54652 standard; cDNA; 1645 BP
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                                                                                                                                                                                                                                                                    T84.12 Heavy chain.
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           1364 GA 1365
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978 CACACAGCTCAGACACACAAACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGC 1037
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                                                                                                                                                                                                                                149 GIGAAGAIGICCIGCAAGGCTICIGGCTACACCTITACTAGGTACACGAIGCACTGGGIA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 CTCCATCAGAGCATGGCTGTTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGT 80
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                                                                                                                                                                                                                                                                                       29 CICTGACTCAACATGGAAAGGCACTGGATCTTTCTACTCCTGTTGTCAGTAACTGCAGGT
                                                                                                                                                                                                                                                                                                                                           258 ACAGACTATAATGCAGCTTTCATAT¢CAGACTGAGCATCAGCAAGGACAATTCCAAGAGC
                                                                                                                                                                                                                                                                                                                                                                 318 CAACTCTTCTTTAAAATGAACAGTC#GCGAGCTACTGACACACCCATATATTACTGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 ACCTCAGTCACCGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCT
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1404 GTGAGACACGAGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGT 1463
                                                                                                                                1464 AAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCATATCCAT 1523
                                                                                                                                                                                                          The OK3T heavy chain sequence was isolated from a cDNA library prepared from OK3T producing cells. The library was screened with a probe complementary to a sequence in the mouse IgG2a constant CH1 domain region. The OK3T sequence was used in CDR-grafting experiments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy and light chains, for use in in vivo therapy and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New humanised antibodies comprising CDR grafted antibody - with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 940.8; DB 12; Length 1570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OK3T; heavy chain; humanised antibodies; CDR-grafting; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1570 BP; 447 A; 443 C; 356 G; 324 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody OK3T heavy chain coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%; Score 940.8; DB 12 77.2%; Pred. No. 4.5e-221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= OK3T heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2a; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emtage JS;
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Query Match

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366 TATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTAC 425
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                         1076 AACAAAGACCTCCCAGCGCCCATCGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGA 1135
                                                                                    1256 GGGAAAACAGAGCTAAAACTACAAGAACACTGAACCTGGACTCTGATGGTTCTTAC 1315
                                                                                                                                                                                                                                                                                                                         1376 TGTTCAGTGGTCCACGAGGGTCTGCACCACCACGACTAAGAGGCTTCTCCCGGACT 1435
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                                                                     1158 GCTCCACAAGTATACATCTTGCCGCCACCAGCAGCAGTTGTCCAGGAAAGATGTCAGT 1217
                                                                                                                              1218 CTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAAT 1277
                                                                                                                                                          1196 CTGACCTGCATGGTCACAGACTTCATGCCTGAAGACATTTACGTGGAGTGGACCAACAAC 1255
                                                                                                                                                                                       1278 GGGCATACAGAGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTAC 1337
                                                                                                                                                                                                                                                1338 TTCATATATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCA 1397
                                                                                                                                                                                                                                                                            1316 TTCATGTACAGCAAGCTGAGAGTGGAAAGAAGAACTGGGTGGAAAGAATAGCTACTCC 1375
                                                                                                                                                                                                                                                                                                         1398 TGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCT 1457
                                                                                                                                                                                                                                                                                                                                                                   1458 CCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCAT 1517
                                                                                                                                                                                                                                                                                                                                                                                                                            1518 ATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAGCCTGGTACCATGTAAAAAAA 1577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anti-snake small neurotoxin antibody; heavy chain; 1gG2;
immunoglobulin; bispecific bivalent antibody; cell-targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody M(alpha)2-3 H-chain coding sequence.
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97 GGAACTGCAGGTGTCCATTGCCAGATCCAGCTGCAGCAGCTGGACCTGAGCTGGTGAAG 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 GTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGT 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from the neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from the chain fragment (VL + CL) was amplified from the same source using primers AAQ48041 and AAQ48042. The two amplified fragments were inserted into the same vector; the H-chain fragment was inserted (in-frame) between codons 6-7 of the phoA coding sequence and the L-chain fragment was inserted into a cassette which contained a phoA S-D sequence, a signal peptide and the first 6 codons of phoA. The cassette was positioned between the transformation codon and the transcription termination sequence of phoA. The fusion construct is expected to to encode a hybrid protein comprising two identical Ab-derived units. The invention also covers hybrid proteins containing two different Ab-derived units (i.e. to produce blobA. The hybrid molecules can be used as cell-targetting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1581;
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tive 0; Mismatches 335; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1581 BP; 435 A; 448 C; 373 G; 325 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boulain J, Ducancel F, Gillet D, Menez A;
                                                                                                                                                                                                                                                                                                                                                                  (COMS ) COMMISSARIAT ENERGIE ATOMIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 3A; 37pp; French.
                                                                                                                                                           93EP-0400323
                                                                                                                                                                                                                                                92FR-0001505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 1207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-260351/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic agents.
                                                                                                                                                                                                                                                                                                                                (BOUL/) BOULAIN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR40384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapeutic use
                                                                                                                                                           09-FEB-1993;
                                                                                                                                                                                                                                                11-FEB-1992;
                                                                                18-AUG-1993.
EP556111-A
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jo i	TATTTCTGTGCCAAGAGCTATGGGGGCTACGGCTACACTTTTGGACTA	4
426	TGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACCCCCATCAGTTTATTTILL	485 504
486	CCACTGGCCCTGGGTGTGGAATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTC	545 564
546 565	AAGGGCTACTTCCCTGAGTCAGTGACTGGACTTGGAACTCTGGATCCCTGTCCAGCAGT	605 624
606	GT6CACACCTTCCCAGGTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTCTACACTATTATTTTTTTT	665 684
999	GTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTGC	725 744
726	AGCACCAGGGTGGACAAAAACTTGAGCCCAGGGGGCCCATTTCAACAATCAACCCCTGT	785 798
786	CCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTC	845 846
846	TTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACG	905 906
906	TGTGTGGTGGTGGTGTGAGCGAGGATGACCCAGACGCCCGATCAGCTGGTTTGTGAC 	965 966
996	AACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGGGTTACAACAGTACTATC	1025 1026
1026	CGGGTGGTCGTCCCCCATCCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAA 	1085 1086
1086	TGCAAGGTCAACAAGAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAA 	1145 1146
1146	GGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGG 	1205 1206
1206	AAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAG	1265 1266
1266 1267	TGGACCAGCAATGGGCATACAGAGGAGAACTACAAGGACACCGCACCAGCTCCTGGACTCT	
1326 1327	GACGGTTCTTACTTCATATATAGCAAGCTCAATATGAAAACAAGCAAG	1385 1386
1386	GATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACC	1445 1446
1446	ATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGAC 	1505 1506

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1506 ACTGGCACCCATATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAGCCTGGTACC 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 CTTGGGGCTGCTCTTCTGCCTGGTGAÇATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic compositions comprising Flt-3 ligand encoding polymuclectide and one or more antigen, or cytokine encoding polymuclectides, useful for suppressing tumour growth and for treating autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of patient-specific bicistronic chimeric idiotype VR1642 (plasmid VAXID), which is used to treat b-cell lymphome patients. The plasmid includes the cytomegalovirus immediate-early promoter, enhancer and 5' untranslated sequences, driving the expression of mouse-human chimeric immunoglobulin light and heavy chain sequences. The human light and heavy chain variable regions are derived from B-cell lymphoma cell line RAMOS. The transcriptional terminator region includes polyA and termination signals from the bovine growth hormone gene. According to the invention, co-administration of VR1642 with a plasmid (see AAF30314) encoding human Fms-like tyrosine kinase (Fit-3 ligand) provides a means of treating a patient with B-cell lymphoma.
                                                                                                                                                                                                                                                                                                                                                                   immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1642;
plasmid VAXID; antibody; idiotype; vector; ss.
                                                                                                                                                                                                                                                                                                                                                Flt-3 ligand; Fms-like tyrosine kinase; mouse; human; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.7%; Score 885; DB 22; Length 7528; 77.8%; Pred. No. 3.5e-207; tive 0; Mismatches 295; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page 101-106; 149pp; English.
                                                                                                                                                                                                                                                                                                               Bicistronic idiotype plasmid VR1642
                                                                                                                                                                                                AAF30316 standard; cDNA; 7528 BP.
                                                                         1566 ATGTAAAAAAAAA 1580
                                                                                         31-JUL-2000; 2000WO-US20679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0146170.
                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Cytomegalovirus.
                                                                                                                                                                                                                                                                         14-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 77.8
Matches 1116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Homo sapiens.
Chimeric - Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200109303-A2.
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                                                                                                                                                                                                                                        AAF30316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188 AACCCATAGAGAGGATTACAACAGTACTCTCCGGGTGGTGGTGAGTGCCCTCCCCATCCAGCGCA 2247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1055 CCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAAAGACCTCCCATC 1114
                                                                                                                                                                                           1426 GCTGGAGTGGATTGGGGAAATCAATCATAGTGGAAGCACCAACTACAACCGTCCCTCAA 1485
                                                                                                                                                                                                                                                                        1486 GAGTCGAGTCACCATATCAGTAGACACGTCCAAGAAGCAGCTCTCCCTGAAGTTGAGCTC 1545
                                                                                                                                                                                                                                                                                                                                  1786 GACCTGGAACTCTGGATCCCTGTCCAGTGGTGTGCACCTTCCCAGCTGTCCTGCAGTT 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1966 CAGAGGGCCC-----ACAATCAAGCCCTGTCCTCCATG------CAAATGCCC 2007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2008 AGCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGT 2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  995 AACCCATAGAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCA 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2248 CCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAACAAGACCTCCCAGC 2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1115 ACCCATCGAGAGCATCTCAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACAT 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2308 GCCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGT 2367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1175 CTTGCCGCCACCAGCAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGT 1234
                                       1306 ACAGCAGTGGGGCGCAGGACTGTTGAAGCCTTCGGAGACCCTGTCCCTCACCTGCGCGGTGT 1365
                                                                                                              1366 TTATGGTGGTCCTTCAGTGGTTACTACTGGAGCTGGATCCGCCAGCCCCCAGGGAAGGG 1425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      575 GACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAGTC 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      755 CAGCGGGCCCATTCAACAATCAACCTGTCCTCCATGCAAGGAGTGTCACAAATGCCC 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   815 AGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGT 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 CGTCACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAACTTGAGCC 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875 ACTCATGATCTCCCTGACACCCCAAGGTCACGTGTGGTGGTGGATGTGAGCGAGGATGA 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 CTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGG 220
                                                                                                                                                      281 ATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAG 340
                                                                                                                                                                                                                                                                                                              341 TCTGCGAGCTACTGACACAGCCATATATTACTGTGCCAGA-----AATAGAGGGGATAT 394
                                                                                                                                                                                                                                                                                                                                                                                       395 TTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  455 CTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAAC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 TGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   635 TGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGAC 694
101 GAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGT 160
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1295 CTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGCAAGCT 1354
                                                                                                                                                                                                                                                                               2488 CTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCT 2547
                                                                                                                                                                                                                                                                                                                                              1355 CAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGA 1414
                                                                                                                                                                                                                                                                                                                                                                          2368 CTTGCCTCCACCAGAAGAAGAAGATGACTAAGAAACAGGTCACTCTGACCTGCATGGTCAC 2427
                                                                                              1235 GGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAA 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 CAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 ACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAGATCCAGTTGGTGCAGTCTGGACCTGAGGAGGCCTGGAGAGACAGTCAAGATC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The DNA encodes the heavy chain of monoclonal antibody KS1/4, used to construct mouse/human chimeric antibodies. KS1/4 is a murine antibody which binds to surface antigens on adenocarcinoma cells and the use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2608 GGGTCTGCACAATCACCACACGACTAGAGCTTCTCCCGGGACTCCGGGTAAATGA 2662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1415 GGGTCTGAAAATTACTACCTGAAGAGACCATCTCCCGGTCTCCGGGTAAATGA 1469
50.5%; Score 801.8; DB 10; Length 1341; 76.9%; Pred. No. 5.7e-187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C regions avoids immunological problems during treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant DNA cpds. producing antibodies - monoclonal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 272; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1341 BP; 371 A; 362 C; 325 G; 283 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KS1/4; chimeric antibody; heavy chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric derived from monoclonal antibody KS1/4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gadski RA, Weigel BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric antibody heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; page 52; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAN91659 standard; DNA; 1341 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.98;
         89EP-0303814.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1063; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ELIL ) ELI LILLY AND CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beavers LS, Bumol TF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-311203/43.
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Dp	QY Db	QQ.	Oy Db	RES AAC ID	DX XX	XX DE	XXX OS OS	X W X C	X X X X X X X X X X X X X X X X X X X	X X X X	X X X Y	PT XX PS	¥8888	S X G	OME	QY	Qy	QY
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CCAGGAAAGGGTCTGGAGTGGTGATATGGAGTGGTGGAGACACAGACTAT 266 	32	TTTAAAATGAACGGTCTGCGAGCTACTGACACAGCCATATTACTGTGCCAGAAAT 383 	AGAGGGATATTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCA 443 	GTCACCGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGT 503	GGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGCTACTTCCCTGAG 563 	TCAGTGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACTTCCCAGCT 623	CTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACTGG 683	CCAAGTCAGACCGTCACCTGCAGGTTGCTCACCCAGCCAG	AAACTTGAGCCCAGCGGGCCCATTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGT 803	CACAAATGCCCAGGTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAT 863 	ATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGGTGGTGGATGTG 923 	AGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACA 983 	GCTCAGACACAAACCCATAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTC 1043 	CCCATCCAGCACCAGGACTGGATGAGGGGGGGTTCAAATGCAAGGTCAACAACAA 1103 	GACCICCCATCACCATGAGAGAACCATCTCAAAATTAAAGGGTAGTCAGAGCTCCA 1163 	CAAGTATACATCTTGCCGCCACCAGCAGTGCCAGGAAAGATGTCAGTCTCACT 1223 	TGCCTGGTCGTGGCCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCAT 1283 	-
210 CCAG 121 CCAG	267 AATGO 1 181 GCTG	327 TTTA 241 TTGC	384 AGAGG	444 GTCAC 337 GTCAC	504 GGAGE 11111 397 GGAGE	564 TCAGI 457 CCAGI	624 CTCCT 517 GTCCT	684 CCAAG 11 11 577 CCCAG	744 AAACT 637 AAAAT	804 CACAA 681CAA	864 ATCAA 739 ATCAA	924 AGCGA 799 AGCGA	984 GCTCA 859 GCTCA	1044 CCCAT 919 CCCAT	1104 GACCT 979 GACCT	1164 CAAGT 1039 CAGGT	1224 TGCCT 1099 TGCAT	1284 ACAGA
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1159 ACAGAGCTAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATG 1218 1179 GTGGTCCAGGAGGTCTGCACAATCACCACAACAACTAAAGAGCTTCTCCCGGACTCCGGGT 1338 1344 TATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAAC 1403 1404 GIGAGACACGAGGGICIGAAAAAITÄCIACCIGAAGAAGACCAICICCCGGICICCGGGI 1463 52 TCTTCTGCCTGGTGACATTCCCAAGGTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAG 111 112 GACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACCAGTTTCT 171 172 CATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGC 231 20 TCCTTTTTCTAGTAGCAACTGCAAGTACATTCASARGTKCAGCTGAAGGAGTCAG 79 Novel anti-death receptor 4 antibodies useful for treating cancer and immune related disorders such as rheumatoid arthritis, sjogren's syndrome, Grave's disease and diabetes mellitus Ouery Match

48.4%; Score 768.2; DB 22; Length 1431;
Best Local Similarity 72.8%; Pred. No. 1e-178;
Matches 1043; Conservative 3; Mismatches 351; Indels 36; Gaps The present invention relates to an anti-Death receptor 4 (DR4) antibody. The antibodies of the invention are useful for inducing apoptosis in mammalian cancer cells such as colon cancer cells and for treating an immune-related disease in a mammal such as arthritis Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis; Sequence 1431 BP; 350 A; 438 C; 367 G; 273 T; 3 other; Dodge KH, Kim KJ; Chimeric 4H6 anti-DR4 antibody heavy chain DNA Disclosure; Fig 18; 126pp; English AAC91017 standard; DNA; 1431 BP Ashkenazi AJ, Chuntharapai A, 25-MAY-2000; 2000WO-US14599. 99US-0322875, 15-MAR-2001 (first entry) and autoimmune disease. (GETH) GENENTECH INC. WPI; 2001-041145/05. 1464 AAA 1466 1339 AAA 1341 WO200073349-A1. 28-MAY-1999; Homo sapiens. 07-DEC-2000. Synthetic. AAC91017; C91017

Db 1199 GCTTCTATCCCAGCGACATCGCCGTGGAGGAGCAATGGGCAGCCGGAGAACAACT 1258 Qy 1297 ACAAGGACACCGCACCTCTCGACTCTTACTTCATATAGCAAGCTCA 1356	RESULT 9 AAC91018/C ID AAC91018 standard; DNA; 1431 BP. X AAC91018; X C CHIMERIC 4H6 anti-DR4 antibody heavy chain complementary DNA. XX Muti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis; X AAC90003349-A1. XX AAC900073349-A1. XX AAC90003349-A1. XX AAC90003349-A1. XX AAC90003349-A1. XX AAC90003349-A1. XX AAC900034000-US14599. XX AAC900034000-US14505. XX AAC900034000-US14505. XX AAC90000-US14505. XX AAC90000-US14505. XX AAC90000-US14506. AAC90000-US14506. AAC90000-US14506. AAC90000-US14506. AAC90000-US14506. AAC90000000-US14506. AAC90000000000000000000000000000000000	Query Match Best Local S Matches 1043 S2 1412	Qy 112 GACCTGGCCTAGTGCAGCCCTCACCACCACCACCACCACCACCACCACCACCACCAC
	11	AGGACTGGATGAGTAGGAAGTTCAAATGCAAGGTCAACAACAAAGAACTCCCATCAC [1177 TGCCGCCACCAGCAGCAGTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGG 1236

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nultimeric complex comprising a first jor histocompatibility complex (MHC) class combinant single chain MHC class II molecule, on a betal domain linked through an timerisation domain. The first and the through the multimerisation domain to form complex is useful for treating autoimmune treating insulin dependent diabetes, is useful forts, pernicious anaemia, autoimmune sumatoid arthritis and systemic lupus sequence encodes a single chain MHC
                                                                                                         AGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGG 1416
TGGAQTCTGACGGTTCTTACTTCATATAGCAAGCTCA 1356
                           ig autoimmune diseases, comprises first
ass II molecules, each comprising alphal
nh amino acid linker and multimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lbility complex; MHC class II; multimer;
/e; antidiabetic; antiinflammatory;
antiarthritic; neuroprotective; vaccine;
apendent diabetes; multiple sclerosis;
anaemia; autoimmune encephalomyelitis;
c lupus erythematosus; ss.
                                                                                                                                                                                                                   AGAAGACCATCTCCCGGTCTCCGGGTAAATGA 1469
                                                                                                                                                                                                                                               À;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nglish
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RESULT 11

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1356 AATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAG 1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              996 ACCCATAGAGAGTTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCAC 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1056 CAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAGACCTCCCATCA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1176 TIGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTG 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1236 GGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGAGGAGAAC 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1015 GCACCTAACCTCTTGGGTGGACCATCCGTCTTCATCTTCCCTCCAAAGATCAAGGATGTA 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1315 CCCATCGAGAGAACCATCTCAAAACCCAAAGGGTCAGTAAGAGCTCCACAGGTATATGTC 1374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1296 TACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGCAAGCTC 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1495 TACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAAGCTG 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1555 AGAGTGGAAAAGAACTGGGTGGAAAGAAATAGCTACTCCTGTTCAGTGGTCCACGAG 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 973 AGAGGGCCC-----ACAATCAAGCCCTGTCCTCCATG-------CAAATGCCCA 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          816 GCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTA 875
                                                                                                                                                                                                                                                       913 ATCACCTGCAATGTGGCCCACCGGCAAGCAGCACCAAGGTGGACAAGAAATTGAGCCC 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756 AGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCA 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     876 CTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGAGTGAGCGAGGATGAC 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                456 TCAGCCAAAACAACCCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACT 515
                                                                                                                                            576 ACTIGGAACTCTGGATCCCTGTCCAGCAGTGTGCCACCTTCCCAGCTCTCCTGCAGTCT 635
                                                                                                                                                                                                                                                                                                                                                                                      793 ACCTGGAACTCTGGATCCCTGTCCAGTGGTGTGCACCTTCCCAGCTGTCCTGCAGTCT 852
                                                                                                                                                                                                                                                                                                                                                                                                                                              636 GGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACC 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         696 GICACCIGCAGCGIIGCICACCCAGCCAGCACCACGGIGGACAAAAAACTIGAGCCC 755
                                                                                                                                                                                                                        516 GGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTG 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1416 GGTCTGAAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGC 1471
                                                           18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.6%; Score 740.8; DB 23; Length 1676; 84.7%; Pred. No. 5.7e-172;
                                                           Indels
                                                        0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                     861; Conservative
                              Best Local Similarity
     Query Match
                                                           Matches
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2854 GACCTTGACCTGGAACTCTGGATCCCTGTCCAGTGGTGTGCACACCTTCCCAGCTGTCCT 2913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 GACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACCACCTTCCCAGCTCTCCT 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 CGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGA 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynuclectide and one or more antigen, or cytokine encoding polynuclectides, useful for suppressing tumour growth and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.5%; Score 737.8; DB 22; Length 6729;
84.3%; Pred. No. 4.7e-171;
Live 0; Mismatches 142; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5' untranslated sequences, driving the expression of mouse immunoglobulin kappa light and gamma 1 heavy chain constant regions. The transcriptional terminator region includes polyA and termination signals from the bovine growth hormone gene. Tumour-specific variable regions from a patient can be PCR amplified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and cloned into this vector to produce the patient's individual vaccine construct. The light and heavy chain variable regions from the B-cell lymphoma cell line RAMOS were amplified and cloned into VR1632 to provide test vaccine construct VR1642 (see AAF30316). According to the invention, co-administration of VR1642 with a plasmid (see AAF30314) encoding human Fms-like tyrosine kinase (Flt-3 ligand) provides a means of treating a patient with B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  includes the cytomegalovirus immediate-early promoter, enhancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of bicistronic plasmid VR1632, which
                                                                                                                                                                             tumour; lymphoma; gene therapy; VR1632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6729 BP; 1727 A; 1744 C; 1629 G; 1629 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic compositions comprising Flt-3 ligand encoding
                                                                                                                                                               Flt-3 ligand; Fms-like tyrosine kinase; mouse; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 107-111; 149pp; English.
                                                                                                                            Bicistronic idiotype plasmid VR1632.
               AAF30341 standard; cDNA; 6729 BP
                                                                                                                                                                                                   antibody; idiotype; vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0146170.
                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2000; 2000WO-US20679.
                                                                                                                                                                                                                                       Chimeric - Cytomegalovirus.
                                                                                      14-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        861; Conservative
                                                                                                                                                                                                                                                        - Mus musculus.
                                                                                                                                                                                  therapy;
                                                                                                                                                                                                                                                                         Chimeric - Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-123319/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VICA-) VICAL INC.
                                                                                                                                                                                                                                                                                                              WO200109303-A2.
                                                                                                                                                                                  immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hermanson GG;
                                                                                                                                                                                                                                                                                                                                                  08-FEB-2001.
                                                    AAF30341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lymphoma.
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                                                                                                                                                                                                                                                            Chimeric
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AAF30341
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                                                      δλ
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g

688 2973	748 3033	808 3075	868 3135	928 3195	988 3255	1048 3315	1108 3375	1168 3435	1228 3495	1288 3555	1348 3615	1408 3675	1468 3735	
9 GCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAG	PTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCACGCACCACGGTGGACAAAAACT) TGACCCCAGGGGCCCATTCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAA 	ATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAA	GGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGTGGATGTGACGA	GGATGACCCAGACTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTACACACAC	GACACAAACCCATAGAGGGTTACAACAGTACTATCCGGGTGGTCAGCACCTCCCCAT	OCACCACGAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACGAAGACCT	OCCATCACCCATCGAGAGAACCATCTCAAAATTAAAGGGCTAGTCAGAGGTCCACAAGT	PARATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCCAGTCTCACTTGCCT 11	GGTCGTGGGCTTCAACCCTGGAGACATCAGTGGGGTGGACCAGCAATGGGCATAAGAGA 	GGAGAACTACAAGGACACCGCCCCGGACCTGACGGTTCTTACTTCATATAGG	CAAGCTCAATATGAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAG 	ACACGAGGGTCTGAAAATTACTACCTGAAGAACACCATČTCCCGGTCTCCGGGTAAATG 	A 1469
629	689 2974	749	809 3076	3136	929 3196	989 3256	1049 3316	1109 3376	1169 3436	1229 3496	1289 3556	1349 3616	1409 3676	1469
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52 TCTTCTGCCTGGTGACATTCCCAAGCTGTGCTCTATCCCAGGTGCAGCTGAAGCAGTCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 GACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 TGGGA---GTGATATGGAGTGGTGGA¢ACACAGACTATAATGCAGCTTTCATATCCAGAC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 TGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTAAAAATGAACAGTCTGCGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 CATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 CCACACTGACTGTAGACAAATCCTCCACCACGCCTACATGCAACTCAGCAGCCTGACAT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       349 CTACTGACACAGCCATATATTACTGT¢CCAGAAATAGAGGGGATATTTACTATGATTTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAD 55.1 (ECACC 93081901) recognises the colorectal tumor-associated antigen CA55.1. CDNAs for the heavy (AAQ94037) and light (AAQ94036) cchains of 55.1 were isolated, and (F(ab)', F(ab)', F(ab)', Fv, scFv or V-min humanized 55.1 constructs have been expressed in myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.4%; Score 720.4; DB 16; Length 1582; 69.2%; Pred. No. 5.7e-167; tive 0; Mismatches 426; Indels 49;
monoclonal antibody; MAD; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin; ss.
                                                                                                                                                                                                                                                                                                                                                              Hall SM, Paterson DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1582 BP; 405 A; 466 C; 379 G; 332 T; 0 other;
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig.15; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                          , Boot C, Copley CG, Wright AF;
                                                                                                                                                                                                                                                                                                     93GB-0024819.
                                                                                                                                                                                                                                                           94WO-GB02610.
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111..1445
/*tag= c
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Matches 1065; Conservative
                                                                                               54..1448
/*tag= a
54..110
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-215262/28.
                                                                                                                                                                                                                                                                                                                                  (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells and E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAR76088.
                                                                                                                                                                                                                                                                                      03-JUN-1994;
                                                                                                                                                                                                                                                           29-NOV-1994;
                                                                                                                                                                                                                                                                                                      03-DEC-1993;
                                                                                                                                                                                                   WO9515382-A
                                                                                                                                                                                                                               08-JUN-1995
                                                                                                                              sig_peptide
                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                                                                                                                                              Blakey DC,
                                                                                                                                                                                                                                                                                                                                                                              Rose MS,
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                                                         Mus sp.
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Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;

MAb 55.1 heavy chain cDNA. 21-NOV-1995 (first entry)

AAQ94037 standard; cDNA; 1582 BP.

ESULT 12 AQ94037 AAQ94037;

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235 GAGTGATATGGAGTGGAGGACACAGACTATAATGC---AGCTTTCATATCCAGACTGA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAP40032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-NOV-1984.
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                  g
                                                      Qγ
                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1309 CACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATACCAAGCTCAATATGAAAACAA 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1369 GCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATT 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1429 ACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCT 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      949 TCAGCTGGTTTGTGAACAACGTGGAAGTACACACAGCTCAGACACAAACCCATAGAGAGG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1009 ATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGA 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    988 AGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCA 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1069 GTGGCAAGGAGTTCAAATGCAAGGTCAACAAAAAGACCTCCCATCACCATCGAGAGAA 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1129 CCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1189 CAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTG 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1249 GAGACATCAGTGTGGACCAGCAATGGGCATACAGAGAGAACTACAAGGACACCG 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1288 AGCCCATCATGGACACAGATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAGAAGA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1348 GCAACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACATGAGGGCCTGCACAACC 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1408 accaracreagaagaccreceacreceggraargareceagreeregrage 1467
                    769 CAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCG 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          829 AGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCC 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                889 TGACACCCAAGGTCACGTGTGTGTGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGA 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868 TGACTCCTAAGGTCACGTGTGTTGTGGTAGACATCAGCAAGGATGATCCCGAGGTCCAGT 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       928 TCAGCTGGTTTGTAGATGATGTGGAGGTGCACACACCTCAGACGCAACCCCGGGAGGAGC 987
409 CTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACGTCTCCTCAGCCAAAACAA 468
                                                                                                                                                                                                                                     589 GATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTA 648
                                                                                                                                                                                                                                                                            604 GATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTC 663
                                                                                                                                                                                                                                                                                                                                                                                                                                      724 TIGCCCACCCGGCCAGCACCACCACGTGGACAAGAAATTGTGCCCCAGGGATTGTGGTT 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 GTAAGCCTTGCATATG-----TACAGTCC 807
                                                                             469 CACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGA
                                                                                                                                                          529 CTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTG
                                                                                                                                                                                                                                                                                                                                                                                             709 TIGCICACCCAGCCAGCACCACCACGTGGACAAAAACTIGAGCCCAGCGGCCCATII
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1468 CTCTGGTCCTACAGGACTCTGACACCTACCTCCACCCCTCCC-TGTATAAATAAAGCACC 1526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CTGGCCTAGTGCCAGCCCTCACAGGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GAGUCUUAAUGGAGCCUGGAGGUCCCUGAAACUCUCCUGUGGAGCCUCUGGAUUCACUU 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 UCAGUAGAUAUGCCAUGUCUUGGGUUCGCCAGACUCCGGAGAAGAGGCUGGAGUGGGUCG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The mRNA is the coding sequence of the combined cDNA inserts of recombinant vectors p gamma 298 and p gamma 11 (see AAN40024).

It encodes gamma anti-carcinoembryonic antigen chain. Using the vectors the immunoglobulin is produced readily in pure monoclonal form. Genetic manipulations can be used to produce chimeras of variants drawing their homology from species differing from each other. Protein manipulation is also possible.
Indels 43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunoglobulin(s) produced by recombinant host cells - useful as antibodies analogous to forms from mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

45.1%; Score 716.8; DB 5; Length 1528;
Best Local Similarity 54.2%; Pred. No. 4.3e-166;
Matches 819; Conservative 231; Mismatches 417; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wetzel RB, Heyneker HL, Riggs AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA encoding gamma anti-carcinoembryonic antigen chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin; ss mRNA; carcinoembryonic antigen chain.
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                                                                                                                Disclosure; Fig. 5A-B; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                      AAN40025 standard; DNA; 1528 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
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973 UCAACAGCACUUGCGCUCAGUCAGUGAACUUCCCAUCAUGCACCAGGACUGGCUCAUUG 1032 952 GCTGGTTTGTGAACAACGTGGAAGTACACAGCTCAGACACAAACCCATAGAGAGGATT 1011 .012 ACAACAGTACTATCCGGGTGGTCAGCACCTCCCCATCCAGCACCAGGACTGGATGAGTG 1071 1072 GCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCATCACCATCGAGAAGCA 1131 1132 TCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAG 1191 1192 AGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAG 1251 1252 ACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGGAGAGAACTACAAGGACACCGCAC 1311 1312 CAGTCCTGGACTCTGACGGTTCTTACTTCATATAGCAAGCTCAATATGAAAACAAGCA 1371 232 CAACCAUUAGUAGUGGUGGUAGUUCACACCUUCCAUCCAGACAGUGUGAAGGGCGAUUCA 291 292 GCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTAAAAATGAACAGTCTGCGAGCTA 351 352 CTGACACAGCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTT 411 412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGCGTCTCCTCCACAGCCAAAACAACAC 471 472 CCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGTACAACTGGTTCCTCCGTGACTC 531 532 TGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGAT 591 592 CCCTGTCCAGCAGTGCACACCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGA 651 652 GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCGTTG 711 712 CTCACCCAGCCAGCACCACGGTGGACAAAAACTTGAGCCCAGCGGGCCCATTTCAA 771 769 AGCCUUGCAUAUG------UACAGUCCCAG 792 772 CAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGG 831 832 GTGGACCATCCGTCTTCATCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGA 891 892 CACCCAAGGICACGIGIGGIGGIGGIGGAIGIGAGCGAGGAIGACCCAAGACGICCAGAICA 951 염 g ⋩ ð ⋩ á ă ð ð

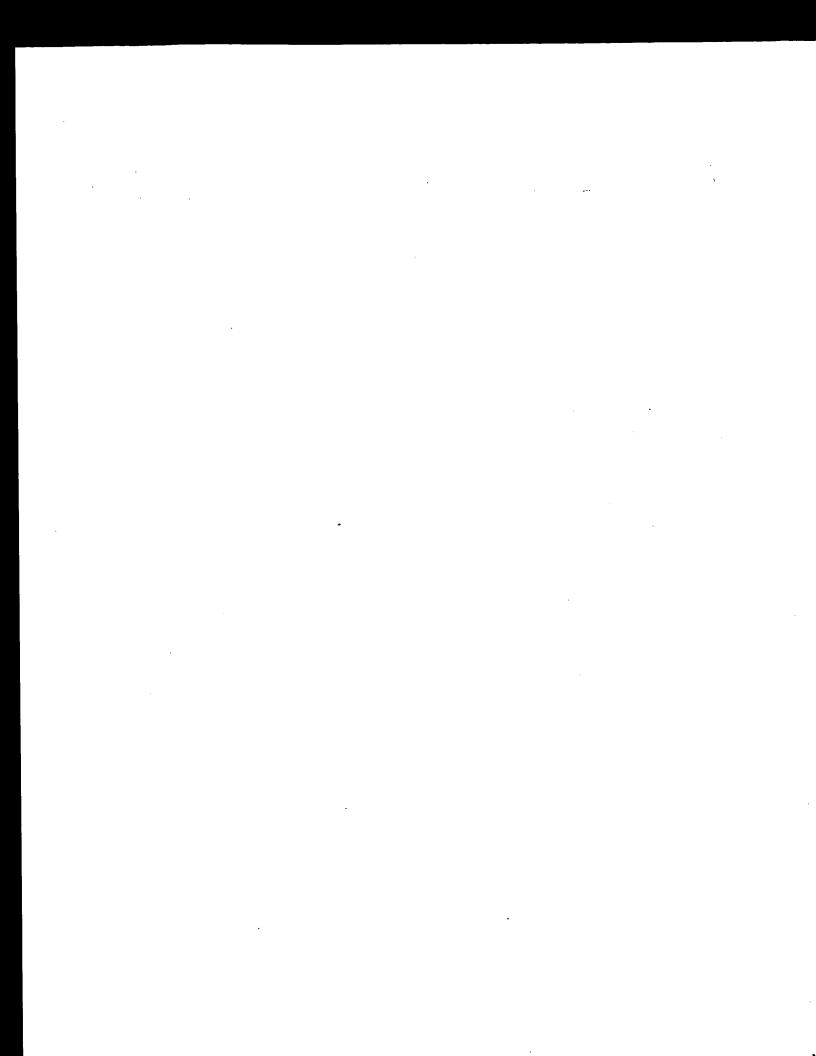
1372 AGTGGGAGAAAACAGATTCCTTCTTCATGCAACGTGAGACACGAGGGTCTGAAAAATTACT 1431 1432 ACCTGAAGAAGACCATCTCCCGGTCIJCCGGGTAAATGAGCTCAGCACCACAAAGGTCTC 1491 1492 AGGTCCTAAGAGACACTGGCACCCAMATCCATGCATCCCTTGTATAAATAAAGCATCCAG 1551 55 TCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114 52 TITACCITGICCITGITITAAAAGITGICCAGIGIGAAGIGAIGCIGGIGGAGICTGGGG 111 115 CTGGCCTAGTGCAGCCCTCACAGAGC¢TGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174 112 GAGTCTTAATGGAGCCTGGAGGGTCCCTGAAACTCTCCTGTGCAGCCTCTGGATTCACTT 171 and p gamma 11. The sequence encodes gamma anti-carcinoembryonic antigen chain. Using the vectors the immunoglobulin is produced readily in pure monoclonal form. Genetic manipulations can be used to produce chimeras of variants drawing their homology from species differing from Indels 43; Gaps Combined cDNA inserts of p gamma 298 and p gamma 11 which encode Immunoglobulin(s) produced by recombinant host cells - useful as The sequence is the combined cDNA inserts of vectors p gamma 298 Query Match
44.9%; Score 713.6; DB 5; Length 1528;
Best Local Similarity 69.4%; Pred. No. 2.7e-165;
Matches 1048; Conservative 0; Mismatches 419; Indels 43; Heyneker HL, Riggs AD; Sequence 1528 BP; 376 A; 443 C; 370 G; 339 T; 0 other; each other. Protein manipulation is also possible. Immunoglobulin; ds DNA; carcinoembryonic antigen; vector p gamma 11; vector p gamma 298. antibodies analogous to forms from mammals. gamma anti-carcinoembryonic antigen chain. Disclosure; Fig. 5A-B; 79pp; English Wetzel RB, AAN40024 standard; DNA; 1528 BP. 83US-0483457. 84EP-0302368 01-DEC-1991 (first entry) 1552 CAAAGCCTGG 1561 Cabilly S, Holmes WE, (GETH) GENENTECH INC. (CITY) CITY OF HOPE. WPI; 1984-283749/46. 06-APR-1984; 08-APR-1983; EP125023-A. AAN40024; RESULT 1 a g g ŏ õ δ g g δ ōλ

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plasmid vector, which was incorporated into A. tumefaciens. The resultant plant expression vector was used to transform tobacco plants, making them TWV resistant, the plants could
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                    352 CTGACACAGCCATATATACTGTGCCAGAAATAGAGGGGATATTACTATGATTTCACTT 411
                                                                                                                                                                                                                                                              352 AGGACACGGCCATGTATTACTGTGCAAGA---CCCCCTCTTATTTCTGTAGTAGCGGACT 408
                                                                                                                                                                                                                                                                                                412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACACA 471
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175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
                                                                          235 GAGTGATATGGAGTGGTGGAGACACAGACTATAATGC---AGCTTTCATATCCAGACTGA 291
                                                                                                              232 CAACCATTAGTAGTGGTGGTAGTTCACACCTTCCAGCAGACAGTGTGAAGGGCGATTCA 291
                                                                                                                                                  292 GCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTCTGCGAGCTA 351
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1393 ATACTGAGAAGAGCCTCTCCCACTCTCCTGGTAAATGATCCCAGTGTCCTTGGAGCCCTC 1452
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                                                                                                                                                                        1273 CCATCATGAACACGAATGGCTCTTACTTCGTCTACAGCAAGCTCAATGTGCAAAGAGAA 1332
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                                                                                                                                                                                                                                                                                                                   1333 ACTGGGAGGCAGGAAATACTTTCACCTGCTCTGTGTTACATGAGGGCCTGCACAACCACC 1392
                                                                                                                                                                                                                                                                                                                                                                                            1432 ACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCCACAAAGCTCTC 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-tobacco mosaic virus monoclonal Ab heavy chain cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      heavy chain; virus-resistant plants; biofarming; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco mosaic virus; TMV; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ79930 standard; cDNA to mRNA; 1553 BP
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973 AAGTACACACACCTCAGACACAAACCCATAGAGGATTACAACAGTACTATCCGGGTGG 1032 159 CTTCAGTGAAGTTGTCCTGCAAGGCTTCTGGCTACACCTTTACTAGCTACTGGATGCAGT 218 196 GGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGAGTGATATGGAGTGG---TG 252 219 GGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGGGCTATTTATCCTGGAAATG 278 373 GIGCCAGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTC 432 76 GCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCAC 135 136 AGAGCCTGTCCAFCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACT 195 253 GAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCA 312 279 GTGATACTAGGTACACTCAGAAGTTCAAGGGCAAGGCCACATTGACTGCAGATAAATCCT 338 313 AGAGCCAACTCTTCTTTAAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACT 372 433 AAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACCCCCCATCAGTCTATCCACTGG 492 CCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCT 552 553 ACTICCCIGAGICAGIGACTGIGACTIGGAACTCTGGAICCCIGICCAGCAGTGIGCACA 612 CCTTCCCAGCTCTCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCT 672 793 GCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCT 852 853 TCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGG 912 913 IGGIGGAIGIGAGCGAGGAIGACCCAGACGICCAGAICAGCIGGIIIGIGAACAACGIGG 972 733 CGGTGGACAAAAAACTTGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCAT 792 837 TCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTTG 896 16 AGAGCCTCCATCAGAGCATGGCTGTCTTGGGGCTGCTTCTGCCTGGTGACATTCCCAA 75 39 AAACACTGACTCTAATCATGGAATGTAACTGGATACTTCCTTTTATTCTGTCAGTAACTT 98 46; Gaps 753 AGGTGGACAAGAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATATG-----Query Match 43.5%; Score 690.6; DB 16; Length 1553; Best Local Similarity 67.7%; Pred. No. 1.2e-159; Matches 1049; Conservative 0; Mismatches 454; Indels 46; also be biofarmed for the prodn. of anti-virus antibodies. Sequence 1553 BP; 386 A; 450 C; 372 G; 345 T; 0 other; 493 엄충 ŏ ă ð ā

1033 TCAGCACCCTCCCCATCCAGCACCAGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGG 1092 1153 TCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGGAGGAGCAGTTGTCCAGGAAAGATG 1212 1137 CGAAGGCTCCACAGGTGTACACCATTCCACCTCCCAAGGAGCAGATGGCCAAGGATAAAG 1196 1213 TCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCA 1272 1197 rcagrergacergeargaraacagachrerrecergaagacarraergragagregeagr 1256 1273 GCAATGGGCATACAGAGGAGAACTACAAGGACACCGCACCAGGTCCTGGACTCTGACGGTT 1332 1317 CITACTICGICIAGAGCAAGGICAAIĢIGAGAAGCAACTGGGAGGCAGGAAAIACIT 1376 1377 TCACCTGCTCTGTGTACATGAGGGCCTGCACCACCATCATGAGAGAGCCTCTCCC 1436 1437 ACTCTCCTGGTAAATGATCATCCCAGTGTCCTTGGAGCCCTCTGGTCCTACAGGACTCTGGAA 1496 1393 TCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCC 1452 1453 GGTCTCCGGGTAAATGAGCTCAGCACÇCAAAAGCTCTCAGGGTCCTAAGAGACACTGGCA 1512 1497 CCTACCTCCACCCTCC-TGTATAAATAAAAGACCCAGCAGCACCAGCCTTG 1544 1513 CCCATATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAGCCTGG 1561 Search completed: June 23, 2003, 20:29:0 ò g qq δλ g ŏ pp δλ g g ò g



June 23, 2003, 16:26:36 ; Search time 4270.96 seconds (without alignments) 10820.814 Million cell updates/sec 1 ccatcotottotcatagago......taaaaaaaaaaaaaaaaa 1588 4109280 Total number of hits satisfying chosen parameters: 2054640 segs, 14551402878 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model Scoring table: IDENTITY_NUC Gapox 10.0 , Gapext 1.0 em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:* em_htg_hum:*
em_htg_inv:*
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em_htg_mus:* em_htg_pln:* em_htg_rod:* em_htg_mam:* Winimum DB seq length: 0

Waximum DB seq length: 200000000 em_htg_vrt:* em_sy:* US-09-770-916-1 1588 gb_sy:*
gb_un:*
gb_vi:*
em_ba:* em_hum: *
em_in: *
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gb_pl:* em_sts:* em_pl:* em_ro:* em_ph:* em_un:* em_vi:* GenEmbl:* Perfect score: Database : Searched: Sequence: Run on: Title:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ES.	Description	27 Mu 47 Mu	. X13188 Mouse	X67210 M.musc	AX466450 Secuence	L00051 Mus musc	AX466448 Seque	BC018365 Mus		BC003888 Mus	A22261 M.m		A77138		X7042	BC031	BCO18	E33134 Humaniz			V00798 Mouse mRN				U17166 Cricet		AX080954 Seque	AJ294738 Mus		AF466769 Mus		T04458 Sequenc E00399 Mouse a	BC002121 Mus m	M.musculus	003334 Mus MusCutu BC003435 Mus muscu	SIN		<pre>bp mRNA linear ROD 07-AUG-2002 IMAGE:2651776, mRNA, complete cds.</pre>			Craniata; Vertebrata; Euteleostomi;	יווד, מעו ועמפי מעו ווומפי	
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ć	% Query Match	77.6																																				BC010327 Mus musculı	10327 10327.1 G	e mouse	Mus musculus Eukaryota; M Mammalia: Fu	1 (bases 1 to Strausberg.R	14:0
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GFTFSDYGMWTRQAPEKGLEWAYINSGSTTIYADTVKGFFTISTDNRKNTLFLLQM
TSLASEDTAMYVCAPEKGLEWAYINSGGTTITVSSAKTTPPSVYPLAFGCGDTTGSSY
TLGGLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVT
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CLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFS
                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found
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                                                                                                                                                                                                                                                                                                                   Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 5 Row: g Column: 12
This clone was selected for full length sequencing because it
                       Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR
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Cancer Genomics Office, National Cancer
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                                                                                                                                                   A Library Preparation: Life Technologies, Inc.
A Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: Baylor College of Medicine Human Genome
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/protein_id="AAH10327.1"
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                                                                                                                                                                                                                                                  Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
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/clone="MGC:6533 IMAGE:2651776"
                                                                                                                                   Tissue Procurement: Gilbert Smith, Ph.D.
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                                                                                                                   Email: cgapbs-r@mail.nih.gov
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    Gene Collection (MGC),
                                                                                            Contact: MGC help desk
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1019 ACAACAGTACTATCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTG 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1012 ACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTG 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1072 GCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCATCACCATCGAGAAACA 1131
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                                                                                                                                                                                                                                                                                                                                                   472 CCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTC 531
                                                                                                                                                                                                                                                                                                                                                                                532 TGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGAT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  592 CCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTGCAGTCTGGACTCTACACTATGA 651
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                                                        317 CCATCTCCAGAGACAATGCCAAGAACACCCTGTTCCTGCAAATGACCAGTCTAAGGTCTG 376
                                                                                                                                                                                                                                  412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACACA 471
292 GCATCAGCAAGGACAATTCCAAGAGCCAACTCTTCTTTAAAATGAACAGTCTGCGAGCTA 351
                                                                                                                 352 CTGACACACCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 TGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTGGAT
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Query Match
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 39 Row: p Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                     1439 ACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTC 1498
                                                                                                                                                                                                                 ACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTC 1491
                                                                                                                                                                                   ROD 07-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Masterins, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV." /clone_lib="NOIL CGAP_Lu29" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BC025447 1578 bp mRNA linear ROD 07-AUG-20
Mus musculus, clone MGC:29400 IMAGE:5068622, mRNA, complete cds.
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Submitted (06-MAR-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                            CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                             1552 CAAAGCCTGGTACCATGTAAAAAAAAAAAAAAAAA 1588
                                                                                                                                                                                                                                                                                                                                              1559 CAAAGCCT--TACCATGTAAAAAAAAAAAAAAAAAA 1593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="C2ECH II"
/clone="MGC:29400 IMAGE:5068622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6"
54. .1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: nisc_mgc@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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DEFINITION

COCUS

RESULT 2 3C025447 ACCESSION

KEYWORDS

SOURCE

/ERSION

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

REMARK

EATURES

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TCSVAHPASSTIVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKD
VLMISLIPRVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSALP
                                                                                                                               /translation="MEWPdILLFLLSVTEGVHSQVQLLQSGPELVKPGASVKISCRAS
GYAFSKSWMWWVRRRPGKGLEWIGRIFPGDGDTHYSGKFQGKAKLIADKSSVTAFLQL
                                                                                                                                                                                                   TSLTSEDSAVYFCARDSDYGDYFDDWGQGATVTVSSAKTTPPSVYPLAPGCGDTTGSS
VTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTWSSSVTVPSSTWPSQTV
                                                                                                                                                                                                                                                                                                                                          IQHQDWWSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSL
TCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 AGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 CCTCAGTGAAGATCTCCTGTAGGGCTTCTGGCTACGCATTCAGTAAGTCCTGGATGAACT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 GGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGTGG---TG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253 GAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCA 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           337 CCGTCACAGCCTTCTTGCAACTCACCAGCCTGACGTCTGAGGACTCTGCGGGTCTATTTCT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 GIGCCAGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTC 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.3%; Score | 1195.8; DB 10; Length 1578; 87.0%; Pred. | No. 1.3e-311; Live 0; Mismatches 182; Indels 18; Gaps
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/protein_id="AAH25447.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1393 TCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCC 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1453 GGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCA 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROD 22-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1213 TCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACTTCA 1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1273 GCAATGGGCATACAGAGGAGAACTACAAGGACACCGCACCCAGTCCTGGACTCTGACGGTT 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1402 TCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCC 1461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            973 AAGTACACACACGCTCAGACACAAACCCATAGAGAGATTACAACAGTACTATCCGGGTGG 1032
                                                                                                                                                                                                                                                                                                                                 1033 TCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGG 1092
                                                                                                                                                                                                                                                                                                                                                                                                                    1093 TCAACAACAAAGACCTCCCATCACCCATCGAGAGAACCATCTCAAAAATTAAAGGGCTAG 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                           1153 TCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAGATG 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                982 AAGTACACACACCTCAGACACAAACCCATAGAGAGATTACAACAGTACTATCCGGGTGG 1041
                                                                                                                                                                                                                                                                                                                                                                          1042 TCAGTGCCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGG 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1222 TCAGTCTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGGACCA 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     913 TGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGG 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                    802 GCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCT 861
                                                              853 TCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGG 912
                                                                                                           862 TCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGG 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Waele, P., Feys, V., Van de Voorde, A., Molemans, F. and Fiers, W. Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MMIGE6H 1579 bp mRNA linear ROD 22-MAI
Mouse mRNA for anti-hPLAP-directed immunoglobulin E6-H chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biochem. 176 (2), 287-295 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1579)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alkaline phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X13188.1 GI:51780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X13188
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Achieved expression in non lymphoid cells.

88329081

JOURNAL MEDLINE PUBMED

SFINITION

SULT 3

4IGE6H

CESSION

SYWORDS

RSION

ORGANISM

URCE

SFERENCE

Location/Qualifiers

SATURES

MMENT

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/translation="MEWINIFLFILSGTAGYOSOYOLOOSGAELARPGASYKLSCKAS
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SSLTSEDSAVYFCAGPRQVGLLPFGYWGGGTLVTASAAKTTPPSYYPLAPGGGTTGS
SVTLGCLVKGYFPESYTVTWNSGSLSSSVHTFPALLQSGLYTMSSSYTVPSSTWPSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTCSVAHPASSTTUDKKLEDSGPTSTINPCPPCKECHKCPAPNLEGGPSVFIFPPNĪK
PVLMISLTPRKTCVVVDVSEDDPDVOJSWFVNNPVLIAOTGVTHREDVNSTIRVVSAL
PIQHODWMSGKEFKCKVNNKDLPAPIERISKIKGIVRAPQVYILSPPPEDLESKENDVS
LICLAVGFSPEDISVEWTSNGHTBENVKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 GTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 AAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACACCCCCATCAGTCTATCCACTGG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493 CCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            553 ACTICCCIGAGICAGIGACIGIGACIIGGAACICIGGAICCCIGICCAGCAGIGIGCACA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             613 CCTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCT 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AGAGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 GGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGTGGGGGTGATATGGAGTG---GTG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 GAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     335 CCAGCACAGCCTACTTGCACCTCAGCAGCCTGACATCTGAGGACTCTGCCGTCTATTTCT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 GIGCCGGACCIAGACAGGICGGGCIACICCCII------IIGGIIACIGGGGCC 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        503 CCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCT 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563 ACTICCCIGAGICAGIGACIGIGACTIGGAACICCGGAICCCIGICCAGCAGIGIGCACA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCAC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 CCTCAGTGAAGCTGTCCTGCAAGGCCTCTGGATACACCCTCACAAGTTATGGTATAAGTT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AGAGCCTCCATCAGAGCATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 ACACACTGACTCTAACCATGGAATGGATCTGGATCTTTCTCTTCATCCTGTCAGGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                      /note="precursor E6-H chain (AA -19 to 456)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109. .1476
/product="mature E6-H chain (AA 1-456)"
/446 c 376 g 340 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSCNVRHEGLKNYYLKKTISRSPGK"
                                                                                                                                                                                                                                                                                                   /protein_id="CAA31580.1"
/db_xref="G1:51781"
                                                                                                  /cell line="E6 hybridoma"
/organism="Mus musculus"
                                                                                                                                                                         /note="pot. start codon"
                                 /db_xref="taxon:10090"
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COCUS

RESULT 4

ACCESSION VERSION

KEYWORDS

Mus musculus

ORGANISM

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/translation="MEWSWIFFLEGGTAGVHSEVQLQQSGPELVNPGASVKMSCKAS
STFITYVMHWVKQREQGLEMIGYTNENKDGFTKGATATLEDKSSNTAYMEL
SSLTSEDSAVYCARDYDYDWFAYWQGGTLYTVYSAAKTTPPSVYPLAPGCGDTTGSSV
TSGCLVKGYFPESVTVTWWSGSLSSSVHTLSQALLQSGLYTMSSSYTVPSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGESVFIFPPNIKD
VLMISLIPWYTVVYVDVSEDDPDVOISMFVNNVEVHTAQTOTHREDVNSTIRVVSTLP
IQHOWWSGREFKCKVNNKFLDSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLL
TCLVVGFNPGDISVEWTSMGHTEENTKDTAFVLDSDGSYFITSKLMMKTSKMEKTDSF
SCNVRHEGLKNYYLKKTI$RSPGK"
Eukaryota; Metazoa; Chordath; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentih; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 AGAGCCTGTCCATCACCTGCACAGTGTCTGGTTTCTCATTAACTAGCTATGGTGTACACT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 GGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGTGGAGTGATATGGAGTGGTGGAG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AGAGCCTCCATCAGAGCATGGCTGTQTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 ACACACTGACTCTAACCATGGAATGGAGTTGGATATTTCTCTTTCTCTGTCAGGAACTG 75
                                                                                                                     Submitted (06-JUL-1992) R. Fischer, Botanisches Inst. (BioI) der RWTH Aachen, Worringer Weg 1, 5100 Aachen, FRG
                                                                                                                                                                 2 (bases 1 to 1546)
Fischer,R., Voss,A., Niersbach,M., Hunziker,W., Hirsch,H.J. and
                                                                                                                                                                                                                                        Production of a Tobacco mosaic virus (TMV) inactivating neotop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.8%; Score 1155.8; DB 10; Length 1546;
85.7%; Pred. No. 8.4e-301;
tive 0; Mismatches 197; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="cDNA H24"
/cell_line="hybridoma (x63-Ag8.165 x spleen cells)"
/tissue_type="spleen"
/clone_lib="puol8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="immunoglobulin gamma 2b heavy chain"
/protein_id="CAA47649.1"
/db_xref="G1:54827
                                                                                                                                                                                                                                                                 specific monoclonal antibody in Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="constant region (gamma 2b)"
1526. .1531
                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="variable region"
                                                                                                                                                                                                                                                                                                                                                                                 /strain="BALB/c"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="leader peptide"
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                                                                                                                                                                                                                                                                                                               Location/Qualifier
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33. .1457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="CDR1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="CDR2 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="CDR3 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                              (bases 1 to 1546)
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437 c
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Best Local Similarity 85.79
Matches 1328; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .194
                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 287
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                                                                                                                                                                                                                  Kreuzaler, F.
                                                                                                                                                                                                                                                                                    Unpublished
                                                                    Fischer, R
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                                              REFERENCE
AUTHORS
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                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                       JOURNAL
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                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1030 TGGTCAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCA 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1150 TAGTCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTTGTCCAGGAAAG 1209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018 IGGICAGCACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCA 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910 IGGIGGIGGAIGIGAGCGAGGAIGACCCAGACGICCAGAICAGCIGGIIIGIGAACAACG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 ACTICCCTGAGTCAGTGACTGTGACTTGGAACTCTGGATCCCTGTCCAGCAGTGTGCACA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              613 C---CTTCCCAGCTCTCCTGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          730 CCACGGTGGACAAAAACTTGAGCCCAGGGGCCCATTTCAACAATCAACCCCTGTCCTC 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          790 CATGCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCA 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           850 TCTTCCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTG 909
                                                                                                                                                                                                                                                                                              433 AAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACACCCCCCATCAGTCTATCCACTGG 492
                                                                                                                                                                                                                                                                                                                                                                                              493 CCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 AC---ACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCA 312
                                                256 ACGGTACAAAGTTCAATGAGAAGTTCAAAGGCAAGGCCACACTGACTTCAGACAAATCCT 315
                                                                                                313 AGAGCCAACTCTTTTAAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACT 372
                                                                                                                                                316 CCAACACAGCCTACATGGAGCTCAGCAGCCTGACCTCTGAGGACTCTGCGGTCTATTACT 375
                                                                                                                                                                                                373 GTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTC 432
                                                                                                                                                                                                                                                376 GIGCAAGAGACTATGATTACGACTGGTTTGCT------TACTGGGGCC 417
                                                                                                                                                                                                                                                                                                                                              418 AGGGGACTCTGGTCACTGTCTCTGCAGCCAAACAACACCCCCCATCAGTCTATCCACTGG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                           478 CCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACCTCTGGGTGCCTGGTCAAGGGCT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           538 ACTICCCIGAGICAGIGACIGIGACTIGGAACICIGGAICCCIGICCAGCAGIGIGCACA 597
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1 (bases 1 to 1113)
Sikorav,J.L., Auffray,C. and Rougeon,F.
Structure of the constant and 3' untranslated regions of the murine Balb/c gamma 2a heavy chain messenger RNA
Nucleic Acids Res. 8 (14), 3143-3155 (1980)
81076554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISTINPCPPCKECHKCPAPNLEGGPSYFIFPPNIKDYLMISLTPKYTCVVVDVSEDDP
DVQISMFVNNYEVHTAQTQTHREDYNSTIRVVSHLPIOHQDWMSGKEFKCKVNNKDLP
SPIERTISKPKGLVRAPQVYTLPPPAEQLSRKDVSLTCLVVGFNPGDISVEMTSNGHT
EENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPEPVTVTWNSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGP
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                  1390 CCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGAACATCT 1449
                                                                                                       1378 CCTTCTCATGCAACGTGAGACACGAGGTCTGAAAATTACTACCTGAAGAAGAACATCT 1437
                                                                                                                                                     1450 CCCGGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTG 1509
                                                                                                                                                                                             1438 cccgrcrccgggraaargagcrcagcacccacaaagcrcrcaggrccraagagacacrg 1497
                                                                                                                                                                                                                                                                                                                                                                                                  ROD 10-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 GCCAAAACAACCCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGT 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               519 TCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
/note="unnamed protein product; Protein sequence is
                                                                                          68.9%; Score 1093.8; DB 10; Length 1113; 98.9%; Pred. No. 4.7e-284;
                                                                                                                                                                                                                                             1510 GCACCCATATCCATGCATCCTTGTATAAATAAAGCATCCAGCAAAGCC 1558
                                                                                                                                                                                                                                                               1498 GCACCCATATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAGCC 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementary DNA; gamma-immunoglobulin; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse mRNA for gamma-2b-immunoglobulin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA24179.1"
/db_xref="GI:1333985"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                    1113 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="exon 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="exon 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              688. .1008
/note="exon 8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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Tue Jul

120	638	698 240	758 300	818 360	878 420	938	998	1058 600	1118 660	1178 720	1238 780	1298 840	1358 900	1418 960	1478	1538	
	TGGAACTCTGGATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTCCTGCAGTCTGGA	CTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTC	ACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAAACTTGAGCCCAGC	GGGCCCATITCAACAATCAACCCTGICCICCATGCAAGGAGTGICACAAAIGCCCAGCT 	CCTAACCTCGAGGGGGACCATCCGTCTTCCTTCCCTCCAAATATCAAGGATGTACTC	ATGATCTCCCTGACACCCAAGGTCACGTGTGTGGTGGTGGTGGTTGTGACGAGGAGGTGACCCA	GACGICCAGAICAGCIGGIIIGIGAACAACGIGGAAGIACACACAC	CATAGAGAGGATTACAACAGTACTCGGGTGGTCAGCACCCTCCCCATCCAGCACCGGTIIIIIIIIII	GACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAAAGGACCTCCCATCACCC	ATCGAGAGAACCATCTCAAAATTAAAGGGCTAGTCAGAGCTCCACAAGTATACATCTG 	CCGCCACCAGCAGAGGAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGCCTGGCCTGGCCTGGCCTGGCCCAGGAAGCAGTGTTGTTTTTTTT	TTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAGGGGAGACTAC 	AAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATATAGCAAGGTCAAT	ATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAAGGTGAGACACGGGGT 	CTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCAC 	CCACAAAAGTICTCAGGTCCTAAGAGACACTGGCACCCATATCCATGCATG	ataaagcatccagcaaagcctggtaccatgtaa 1571
61	579	639	699	759 301	819 361	879	939	999	1059	1119	1179	1239 781	1299	1359	1419	1479	1539
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PAT 16-JUL-2002 2, 91 AGGIGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCA 150 151 CCTGCACAGTCTCTGGTTTCTCATTAACTAGGTGTACACTGGGTTCGTCAGTCTC 210 62 CCTGCAGGACTTCTGCATACACATTCACTGAAAACACCGTGCACTGGGTGAACAGAGCC 121 211 CAGGAAAGGGTCTGGAGTGGCTGGGAGTGATATGGAGT---GGTGGAGACACAGACTATA 267 268 ATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTCT 327 182 GCCCGAAGTICAAGGGCAAGGCCACALTGACTGTAGACAAGTCCTCCAGCACAGCCTACA 241 328 TIAAAAIGAACAGICIGCGAGCIACIGACACAGCCAIAITAITACIGIGCCAGAAAIAGAG 387 388 GGGATATTTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCA 447 448 CCGTCTCCTCAGCCAAAACAACACCCCCCCCCCCTGGGTGTGGGG 507 508 ATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAG 567 568 TGACTGTGACTTTGGAACTCTGGATCCCTGTGCAGTGTGCACACCTTCCCCAGCTCTCC 627 688 GTCAGACCGTCACCTGCAGCGTTGCTCACCCAGCCAGCACCACGGTGGACAAAAAAC 747 584 GICAGACCGICACCIGCAGCGITGCICACCCAGCCAGCACCACGGIGGACAAAAAC 643 /organism="synthetic construct"
/db_xref="taxon:32630"
/note="cDNA for heavy chain of recombinant antibody with 628 TGCAGTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAA 687 2 AGTCCAGCTGCARCAGTCTGGACCTGAACTGGTGAAGCCTGGGGCTTCAGTGATGATAT 61 A recombinant monoclonal antibody to phosphotyrosine-containing 68.3%; Score | 1084; DB 6; Length 1389; 87.2%; Pred. No. 2.1e-281; tive 1; Mismatches 156; Indels 21; Gaps 1 others linear Esinger, D., Stiles, L., Lamarche, A. and Jelinek, T. DNA 289 t 3'-histidine tag sequence" 395 c 335 g 289 t Patent: WO 0218443-A 3 07-MAR-2002; UPSTATE BIOTECHNOLOGY, INC. (US) Sequence 3 from Patent WO0218443. 1389 bp Location/Qualifiers 1. .1389 AX466450.1 GI:21899963 synthetic construct artificial sequences. synthetic construct. Matches 1218; Conservative Best Local Similarity proteins AX466450 Query Match source DEFINITION ORGANISM BASE COUNT ACCESSION VERSION REFERENCE AUTHORS JOURNAL KEYWORDS AX466450 ORIGIN qq οy δŏ ò qq g δ qq δy g δ qq q δy ŏ q Qγ QΩ ò

748 ITGAGCCCAGGGGCCCATITCAACAATCAACCCCTGTCCTCCATGCAAGGAGTGTCACA 807

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ligG-2b can be either secreted or membrane-bound. The difference between the two forms lies in the C-terminal peptides. The secreted tail is encoded immediately 3' to the C-gamma-2b-3 domain. The membrane-bound tail is encoded about 1.3 kb 3' to the same domain and is expressed via alternative mRNA splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLIPKVTCVVVDV
SEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDMMSGKEFKCKVN
NKDLPSPIERTISKIKGLVRAPQVYTLPPPAEQLSRKDVSLTCLVVGFNPGDISVEWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEWICDIYPGGGTTUNNENFRGKATLTADTSSSTAYMQLSSLTSEDSAIYHCARGIYY
NSSPYFDSWGGGTTLIVSSAKTTPPSVYPLAPGCGDTTGSSVTSGCLVKGYFPEPVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="EVQLQQSGAELVRPGTSVKMSCKAAGYTFTNYWIGWVKERPGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKL
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Tucker, P.W., Marcu, K.B., Newell, N., Richards, J. and Blattner, F.R. Sequence of the cloned gene for the constant region of murine gamma 2b immunoglobulin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 ACTICCCTGAGTCAGTGACTGTGACTIGGAACTCTGGATCCCTGTCCAGCAGTGTGCACA 612
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                                                                                                                                                       Jesses 1 to 1171)
Zakut,R., Cohen,J. and Givol,D.
Cloning and sequence of the CDNA corresponding to the variable region of immunoglobulin heavy chain MPC11
Nucleic Acids Res. 8 (16), 3591-3601 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin heavy chain MPC11 Nucleic Acids Res. 8 (16), 3591-3601 (1980)
                                                                                                                                                                                                                                                                                                                                                                                    Cloning and sequence of the cDNA corresponding to the variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The first 53 bp of [2] are a cloning artifact (F.R. Blattner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Ig heavy chain variable region gamma-2b
C-region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 1171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="MPC11 myeloma"
join(L00050.1:<1. .364,63. .1072)
                                                                                                                                                                                                                                                                                                                                                                                                         region of immunoglobulin heavy chain MPC11
Nucleic Acids Res. 8, 4839-4839 (1980)
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/db_xref="GI:387221"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROD 10-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048 TCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAACAAGACC 1107
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 164 to 1171)
                                                                                                                                                                                                                                                                                                                                                                                                                      808 AATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCTTCCCTCCAAATATCA 867
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156 ACTT 613 CCTT 1111 216 CCTT	673 CCAG 276 CCAG	733 CGGT(336 CGGT(793 GCAA 396 GCAA	853 TCCC 456 TCCC	913 TGGT 516 TGGT	973 AAGT 576 AAGT	033 TCAG 636 TCAG	093 TCAA 696 TGAA	153 TCAG 756 TCAG	213 TCAG 816 TCAG	273 GCAA 876 GCAA	333 CTTA 936 CTTA	393 TCTC 996 TCTC	453 GGTC 056 GGTC	513 CCCA' 116 CCCA'
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91 AGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCA 150
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                                                                Esinger, D., Stiles, L., Lamarche, A. and Jelinek, T. A recombinant monoclonal andibody to phosphotyrosine-containing
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                                                                                                                                                                                                                                                                                             / Match 68.1%; Score 1081.2; DB 6; Length 1365; Local Similarity 87.6%; Pred, No. 1.2e-280; nes 1211; Conservative 1; Mismatches 149; Indels 21;
                                                                                                                                                                                         /organism="synthetic construct"
/db_xref="taxon:32630"
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                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1348 GCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGA 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1304 GACACGAGGGTCTGAAAAATACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAT 1363
                                                                                                                                                                                                                                                                                                                           1108 TCCCATCACCCATCGAGAGCCATCTCAAAAATTAAAGGGCTAGTCAGAGCTCCACAAG 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                  1004 TCCCATCACCCATCGAGAGAACCATCTCAAAATTAAAGGCCTAGTCAGAGCTCCACAAG 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1168 TATACATCTTGCCGCCCACCAGCAGAGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCC 1227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1228 TGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAG 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1124 TGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAATGGGCATACAG 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1288 AGGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTTCTTACTTCATATA 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1184 AGGAGAACTACAAGGACACCGCACCAGTCCTGGACGGTTCTTACTTCATATATA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1244 GCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGA 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1408 GACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCCGGGTAAAT 1467
                                                                                                                                                                                                    988 AGACACAAACCCATAGAGGATTACAACAGTACTATCCGGGTGGTCAGCACCCTCCCCA 1047
                                                                                                                                                                                                                                                                                                   1048 TCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAAAGACC 1107
                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1653)
                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-DEC-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
868 AGGATGTACTCATGATCTCCCTGACACCCCAAGGTCACGTGTGTGGTGGTGGTGTGTGAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC018365.1 GI:17390851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1364 GA 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1468 GA 1469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FINITION
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SULT 9 018365 YWORDS

RSION

REMARK

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VLMISLSPMYTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALP
IQHQDMMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVLPPPAEEMTKKEFSL
TCMITGFLPAEIAVDWISNGRTEQNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSIKSEDTAMYYCSROGVWPFRGFAYWGQGTLVTVSAAKTTAPSVYPLAPVGGTTGS
SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWPSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITCONVAHPASSIKVDKKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKD
                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTLGLSLIFLVLVLKGVQCEVKMVESGGGLVKPGGSLKLSCTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFTFSSYDMSWVRQTPEKRLEWVATISGGGSYTYYPDSVKGRFTISRDNAKNTLFLHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 ATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 TCTGCCTGGTGACATTCCCAAGCTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 GAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTCTCTGTACAGCCTCTGGATTTACCT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 TCAGTAGTTATGACATGTCTTGGGTTCGCCAGACTCCGGAGAGGGCTGGAGTGGGTCG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352 CIGACACAGCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCACTT 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 CTGGCCTAGTGCCAGCCTCACAGGCCTGTCCATCACCTGCACAGTCTCTGGTTTCTCAT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 TAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235 GAGTGATATGGAGTGGTG---GAGACACAGACTATAATGCAGCTTTCATATCCAGACTGA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 GCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTCTGCGAGCTA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 CCATCTCCAGAGACAATGCCAAGAACACCCTGTTCCTACACATGAGCAGTTTGAAGTCTG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 AGGACACAGCCATGTATTACTGTTCAAGACAGGGGGTATGGCCCTTTAGGGGGTTTGCT- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Similar to immunoglobulin heavy chain 1 (serum
                                                                                                                                                                                                                                                            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 23 Row: o Column: 12
                                                                                        Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M. Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                         This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.4%; Score 975; DB 10; Length 1653; 78.7%; Pred. No. 5.5e-252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 310; Indels
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MGC:18751 IMAGE:4009847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pcMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Lu30"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAH18365.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACSVVHEGLHNHLTTKTISRSLGK'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GI:17390852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="CZECH II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1496
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CACTGTCTCTGCAGCCAAACAACAG 501	AGGTACAACTGGTTCCTCCGTGACTC 531	CAGTGACTGTGCAACTCTGGAT 591 	CCTGCAGTCTGGACTCTACACTATGA 65 	AAGTCAGACCGTCACCGCGGTG 711 	AGCCCAGCGGCCCATTCAA 77 	CAAATGCCCAGCTCCTAACCTCGAGG 831 	CAAGGAIGTACTCATGATCTCCCTGA 891 	CGAGGATGACCCAGACGTCCAGATCA 951 	TCAGACACAAACCCATAGACAGGATT 1011 	CATCCAGCACCAGGACTGGATGAGTG 1071 	CCTCCCATCACCATCGAGAACCA 1131 	AGTATACATCTTGCCGCCACCAGCAG 1191 	CCTGGTCGTGGGCTTCAACCCTGGAG 1251 	AGAGGAGAACTACAAGGACACCGCAC 1311 	TCATATATAGCAAGCTCAATATGAAAACAAGGA 1371 	GACACCACGAGGTCTGAAAAATTACT 1431 	NTGAGCTCAGCACCACAAAGCTCTC 1491 	CATCCCTTGTATAAATAAAGCATCCAG 1551
3TACTGGGGCCAAGGGACTCTGGT	2 CCCCATCAGTCTATCCACTGGCCCTGGGTGTGG 	TGGGATGCCTGGTCAAGGGCTACTTCCCTGAGT	CCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCT 	GCAGCTCAGTGACTGTCCCTCCAGCACCTGGCC	CTCACCCAGCCAGCACCACGGTGGACAAAAATTG 	CAATCAACCCTGTCCTCCATGCAAGGAGTGTCACI	GTGGACCATCCGTCTTCATCTTCCTCCTCCAAATAT	CACCCAAGGTCACGTGTGTGGTGGTGGATGTGAGGTGTGAGTGTGAGGTGTGAGGTGTGTGTGTGTGTGTGTGTGTGGTG	GCTGGTTTGTGAACAACGTGGAAGTACACACACAC 	ACAACAGTACTATCCGGGTGGTCAGCACCCTCCC	GCAAGGAGTTCAAATGCAAGGTCAACAACAAAGAC 	TCTCAAAATTAAAGGGCTAGTCAGAGCTCCACAAGT 	AGCAGTTGTCCAGGAAAGATGTCAGTCTCACTTGC 	ACATCAGTGTGGAGTGGACCAGCAATGGGCATACF 1	CAGTCCTGGACTCTGACGGTTCTTACTTCATAIN	AGTGGGAGAAAGAGATTCCTTCTCATCCAACGTC	ACCTGAAGAAGACCATCTCCGGGTCTCCGGGTAAATGA 	AGGTCCTAAGAGACACTGGCACCCATATCCATGCA
453	472	532	592	652	712	772	832	919	952	1012	1072	1132	1192	1252	1312	1372	1432	1492

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ROD 07-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYTFTDHAIHWUQREDGLUMIGYIYPRDDSTKYNEKFKGRATLTARKSSSTAYMOR
NSLTSEDSAVYFCARGGNYWYFDVWGAGTTVTVSSAKTTAPSVYPLAPVGGTYGSSV
TLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWPSQTIT
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QDWMSGREBEKKKNNRALPESFIEKTISKPRGPVRAPQYYVLPPPABERYTKREFSLTC
MITGFLPAETAVDMYSGRFEDNYKNTATVLDSDGSYFMYSKLRVQKSTWERGSLFAC
SVVHEGLHNHLTTKTISRSLGK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1564)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNVAHPASSTKVDKKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P. Garcial, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Similar to immunoglobulin heavy chain 1 (serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (19-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 23 Row: o Column: 23
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                               Mus musculus, Similar to immunoglobulin heavy chain (serum IgG2a), clone MGC:18984 IMAGE:4011654, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                  1552 CAAAGCCTGGTACCATGTAAAAAAAAAAAAAAAA 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/map="CZECH II"
/clone="MGC:18984 IMAGE:4011654"
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Clone distribution: MGC clone distribution information can be found
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1423 AAAATTACTACCTGAAGAAGACCATCTCCCGGTCTCCGGGTAAATGAGCTCAGCACCCAC 1482
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978 GAGAGGATTACAACAGTACTCTCCGGGTGGTCAGTGCCCTCCCCATCCAGCACCAGGACT 1037
                                                                          1063 GGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAAGACCTCCCATCACCATCG 1122
                                                                                                                1038 GGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAACAACAGAGCCCTCCCCATCCCCATCG 1097
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mus musculus, clone MGC:18977 IMAGE:4007264, mRNA, complete cds.
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GYTFTSYWMHWYRQRRQGGLEWIGNINPNSGGTNYNBREFKNRATLAVDKSSSTVYMQL
SSLTSEDSAVYYCTRGYGYDDVYFDVWGAGTTVTVSSAKTTAPSYYPLAPVCGGTTGS
SVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWPSQT
ITCNVAHPASSTKVDRKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPRSRM
                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGWNCIILFLVATATGVHSQVQLQQPGAELVKPGASVKLSCKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 TCTTCTGCCTGGTGACATTCCCAAGCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCACCTGCACAGTCTCTGGTTTCT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 GGGCTGAACTGGTGAAACCTGGGGCTTCAGTGAAGTTGTCCTGCAAGGCTTCTGGCTACA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 CCTTCACCAGCTACTGGATGCACTGGGTGAAGCAGAGGCGTGGACAAGGCCTTGAGTGGA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 TGGGA---GIGATATGGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATATCCAGAC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 TGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTCTGCGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 CCACACTGGCTGTAGACAAATCCTCCAGCACGTATCATCATGCAACTCAGCAGCCTGACAT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 CITAIGCCAIGGACIACIGGGGICAAGGAACCICAGICACCGICICCICAGCCAAAACAA 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 CAGCCCCATCGGTCTATCCACTGGCCCCTGTGTGGAGGTACAACTGGCTCCTCGGTGA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 CTACTGACACAGCCATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATGATTTCA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 CACCCCCATCAGTCTATCCACTGGCCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGAACTCTG 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 CTGAGGACTCTGCGGGTCTATTACTGTACAAGAGGATATGGTTACGACGACGTTTACTTC- 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTGGGATGCCTGGTCAAGGGCTACTTCCCTGAGTCAGTGACTGTGACTTGGAACTCTG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCCCTGTCCAGCAGTGTGCACACCTTCCCAGCTCTGCAGTCTGGACTCTACACTA 648
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 23 Row: n Column: 4
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                  /tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 TIGGAAATATTAATCCTAATAGTGGTGGTACTAACTACAATGAGAAGTTCAAGAACAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.8%; Score 950; DB 10; Length 1594; 78.0%; Pred. No. 3.1e-245; tive 0; Mismatches 320; Indels 19,
                                                                                                                                                                                                                                                                                                                                                                     /product="Unknown (protein for MGC:18977)"
/protein_id="AAH12207.1"
/db_xref="GI:15126552"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECH II"
/clone="MGC:18977 IMAGE:4007264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 t
                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Lu30"
                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 g
                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                              identity to protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 78.0
Matches 1201; Conservative
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949 TCAGCTGGTTTGTGAACAACGTGGAAGTACACACACGCTCAGACACAAAACCCATAGAGAGG 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1003 ATTACAACAGTACTCTCCGGGTGGTGAGTGCCCTCCCCATCCAGCACCAGGACTGGATGA 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1123 CCATCTCAAAACCCAGAGGGCCAGTAAGAGCTCCACAGGTATATGTCTTGCCTCCACCAG 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1189 CAGAGCAGTTGTCCAGGAAAGATGTdAGTCTCACTTGCCTGGTCGTGGGGTTCAACCTG 1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1183 CAGAAGAGATGACTAAGAAAGAGTTCAGTCTGACCTGCATGATCACAGGCTTCTTACCTG 1242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1249 GAGACATCAGTGGGGGGGGCGCAGGAATGGGCATACAGAGGAGAACTACAGGAGGACCG 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1243 CCGAAATTGCTGTGGACTGGACCAGQAATGGGCGTACAGAGCAAAACTACAAGAACACCG 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1309 CACCAGTCCTGGACTCTGACGGTTCTTACTTATAGCAAGCTCAATATGAAAACAA 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1369 GCAAGTGGGAGAAAACAGATTCCTTCTCATGCAACGTGAGACACGAGGGTCTGAAAATT 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1363 GCACTTGGGAAAGAGGAAGTCTTTTCGCCTGCTCAGTGGTCCACGAGGGTCTGCACAATC 1422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1429 ACTACCTGAAGAAGACCATCTCCGGGTCAAATGAGCTCAGCACCCACAAAGCT 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus, Similar to RIKEN cDNA 11near ROD 07-AUG-2002 Mus musculus, Similar to RIKEN cDNA 1810060009 gene, clone MGC:6740 BC003888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1303 CAACAGTCCTGGACTCTGATGGTTCTTACTTCATGTACAGCAGGTCAGGGTACAAAGA 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1423 ACCTTACGACTAAGACCATCTCCCGGTCTCTGGGTAAATGAGCTCAGCACACAATGCT 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    828
                                                                                                                                                                                                                                                                                        823
                          TGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCTGCAGCG
                                                                                                           TIGCTCACCCAGCAGCACCAC¢GTGGACAAAAAACTTGAGCCCAGCGGGCCCATTT
                                                                                                                                        769 CAACAATCAACCCCTGTCCTCCATG¢AAGGAGTGTCACAAATGCCCAGCTCCTAACCTCG
                                                                                                                                                                                                                                                        765 -AACACAGAACCCCTGTCCTCCACTGAAAGAGTGTCCCCCATGCGCAGCTCCCAA
                                                                                                                                                                                                                                                                                                                                       829 AGGGTGGACCATCCGTCTTCATCTT¢CCTCCAAATATCAAGGATGTACTCATGATCTCCC
                                                                                                                                                                                                                                                                                                                                                                   824 TGGGTGGACCATCCGTCTTCATCTTQCCTCCAAG-ATCAAGGATGTACTCATGATCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACACCCAAGGTCACGTGTGTGTGTGTGATGTGAGCGAGGATGACCCAGACGTCCAGA
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ORGANISM

YWORDS

AUTHORS JOURNAL

TITLE

REMARK

MMENT

FERENCE

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1183 CACCAGCAGAGGAGTTGTCCAGGAAAGATGTCAGTCTCACTTGCCTGGTCGTGGGCTTCA 1242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        870 TCTCCCTGAGCCCCATGGTCACATGTGTGTGGTGGATGTGAGCGAGGATGACCCCAGATG 929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              768 cc----acaarcaagcccrgrccrccarg------caaargcccagcaccra 809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  583 ACTCTGGATCCCTGTCCAGCAGTGTGCACCTTCCCAGCTCTCCTGCAGTCTGGACTCT 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643 ACACIATGAGCAGCICAGTGACTGTCCCCTCCAGCACCTGGCCAAGTCAGACCGTCACCT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 823 ACCICGAGGGIGGACCAICCGICTICAICIICCCICCAAAIAICAAGGAIGIACICAIGA 882
                                                                                                                                                                                                                              283 CCAGACTGAGCATCAGCAAGGACAATTCCAAGAGCCAACTCTTTTAAAATGAACAGTC 342
                                                                                                                                                                                                                                                                                  288 GCAAGGCCACATTGACTGCAGATAAATCCTCCAGCACTGCCTACATGCAGCTCAACAGCC 347
                                                                                                                                                                                                                                                                                                                                           343 IGCGAGCTACTGACACACACATATATTACTGTGCCAGAAATAGAGGGGATATTTACTATG 402
                                                                                                                                                                                                                                                                                                                                                                                               348 TGACATCTGAGGATTCTGCAGTGTGTTTCTGTTCAAGAGGGGGATCCATCTACTATGGTT 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 ACGGCCTCTACTATGACTACTGGGGCCAAGGCACCACTATCACAGTCTCCTCAGCCA 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 CGGTGACTCTAGGATGCCTGGTCAAGGGTTATTTCCCTGAGCCAGTGACCTTGACCTGGA 587
166 GITICTCATTAACTAGCTATGGTGTACACTGGGTTCGTCAGTCTCCAGGAAAGGGTCTGG 225
                                                   168 GCTACACCTTCACTGACCATACTATTCACTGGGTGAAGCAGAGGCCTGAACAGGGCCTGG 227
                                                                                                            226 AGTGGCTGGGAGTGATAT---GGAGTGGTGGAGACACAGACTATAATGCAGCTTTCATAT 282
                                                                                                                                                                  228 AATGGATTGGATATATTTATCCTAGAGATGGTAGTACTAAGTACAATGAGAAGTTCAAGG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  403 ATTICACTIATGCCATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEWSWVFLFFLSVTTGVHSOVOLOQSDAELVKPCASVKISCKVS
GYTFTDHTIHWVKQRPEQGLEWIGYIYPRDGSTKYNEKFKGKATLTADKSSSTAYMQL
NSLTSEDSAVCFCSRGGSIYYGYGLYYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGSSVTLGCLVKGYPPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTW
PSQSITCNVAHPASSTKVDKKIEPRGPIIKPCPPCKCPAPNLLGGPSVFIFPPKIKDV
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OHQDMMSGKEFKCKVNNKALPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKKQVTLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GGGTCTTTCTTCTTCTTCCTGTCAGTAACTACAGGTGTCCACTCCCAGGTTCAGCTGCAAC 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 AGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATCACCTGCACAGTCTCTG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108 AGTCTGACGCTGAGTTGGTGAAACCTGGAGCTTCAGTGAAGATTTCCTGCAAGGTTTCTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 9430

Meb 31te: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
                                                                                                                                                                                                                                          Direct Submission
Submitted (28-FEB-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                             Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.5%; Score 944.4; DB 10; Length 1620; 77.2%; Pred. No. 1e-243; tive 0; Mismatches 331; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Similar to RIKEN cDNA 1810060009 gene"
/protein_id="AAH03888.1"
                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="MGC:6740 IMAGE:3590907"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Lu29"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                      BC003888.1 GI:13278068
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: MGC help desk
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                                                                                                                                                                                                                         Strausberg, R.
                                                                                                            Mus musculus
                                                                             house mouse.
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Source

Query Match

ASE COUNT

1230 TGCCTGAAGACATTTACGTGGAGTGGACAACAAGGGAAAACAGAGGCTAAACTACAAGA 1289 1303 ACACGCACCAGTCTGGACTCTGACGGTTCTTACTTCATATAGGAAGCTCAAATATAA 1362	qo a	09 AAACAGAGGCCIGGACAGGGTCGGATGGATACATTAATCCTAGCCGTGGTTAT 26
ATGA 135 CTGG 134	do do	258 ACAGACTATAATGCAGCTTTCATATGCAGCAGGACTAGGAGCAAGGACAATTCCAAGAGC 317
AAACAAGCAAGTGGGAGAAAACAGATTCCTTCATGCAACGTGAGACACGAGGTCTGA 1422 	QY	318 CAACTCTTTTAAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACTGTGCC 377
1423 AAAATTACTACCTGAAGAAGACCATCTCCGGGTTCCGGGTAAATGAGCTCAGCACCCAC 1482 	, yo	378 AGAAATAGGGGATATTACTATGATTTCACTTATGCCATGGACTACTGGGGTCAAGGA 437
1483 AAAGCTCTCAGGTCCTAAGAGACACTGGCACCCATATCCATGCATG	QV DP	438 ACCTCAGTCACCGTCTCCTCAGCAAAACAACCCCCATCAGTCTATCCACTGGCCCCT 497
1543 AGCATCCAGCAAGCCTGGTACCATGTAAAAAAAAAAAAA	, dq	498 GGGIGTGGAGATACAACTGGTTCCTGGGATGCCTGGTCAAGGCTTC 557
6] 1570 hr Må linger pam 00. mm	do Db	558 CCTGAGTCAGTGACTTGGAACTCTGGATCCCTGTCCAGAGTGCACACACTTC 617
	da oy	618 CCAGCTCTCCTGCAGTCTGACTTTGACTAGCAGCTCAGTGACTGTCCCCTCCAGC 677
ostomi	QY	678 ACCTGGCCAAGTCAGACCGTCACCTGCAGCGTGCTCACCCAGCAGCAGCACCAGGGG 737
Location/Qualifiers 1. 1570 // Organism - Mus musculus / / / / / / / / / / / / / / / / / / /	δο O	738 GACAAAAAACTTGAGCCCAGCGGCCCATTTCAACAATCAACCGTGTCCTCCATGCAAG 797
41. 1447 /codon_start=1 /product="OKT3 heavy chain" /protein id="CAA01595 1"	Qy Dp	798 GAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGTGGACCATCCGTCTTCATCTTCCCT 857
/db_xref="G1:21727144" //db_xref="G1:21727144" //db_xref="G1:21727144" //db_xref="G1:21727144" //db_xref="G1:21727144" //db_xref="G1:21727144" //db_xref="G1:21727144" //db_xref="G1:21727144" //db_xref="G1:2172714" //db_xref="G1:2	. VQ	858 CCAAATAICAAGGAIGIACICAIGAI <mark>CICCCIGACACCCAAGGICACGIGIGIGGIGGIG 917</mark>
VTLGCLVKGYPPEDVYTTWROSSLSGWYDYDDAYDDAYDGWYDSTWPSOGY YTLGCLVKGYPPEDVYTTWROSSLSGWYDTPPAVLQSDLYTLSSSWYYTSGWPSOGY TCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISL SPIYTCVVVDVSEDDDDVQISWFVWYNSFWYHRAGYDGHREDNSTERKVSALPIQDW MSGREFKCKVNNKDLDADIPPTISCPKGSVDADADOXVVYDDDDPPEDWYWYGYWYN	QY Db	918 GATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 977
FMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVH EGLINHHTTKSFSRTPGK" 447 a 443 c 356 g 324 t	ζς.	978 CACACAGCTCAGACACAAACCCATAG <mark>AGAGATTACAACAGTACTGTCGGGTGGTCAGC 1037</mark>
ttch 59.2%; Score 940.8; DB 6; Length 1570; 241 Similarity 77.2%; Pred. No. 9.5e-243; 1210; Conservative 0; Mismatches 322; Indels 36; Gans 4.	yo d	1038 ACCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1097
ACATGGCTGTTTGGGGCTGCTTCTGCCTGGTGACATTCCCAAGCTGT 80	Qy	1098 AACAAAGACCTCCCATCACCATCGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGA 1157
	Qy	1158 GCTCCACAAGTATACATCTTGCCGCCACCAGAGCAGTTGTCCAGGAAAGATGTCAGT 1217
20.	Qy	1218 CTCACTTGCCTGGTCGTGGGCTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGCAAT 1277
	δ	1278 GGGCATACAGAGAGAACTACAAGAQACCGCACCAGTCCTGGACTCTGACGGTTCTTAC 1337

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733 CGGTGGACAAAAAACTTGAGCCCAGCGGGCCCATTTCAACAATCAACCCCTGTCCTCCAT 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1210; Conservative
                                            .1456
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ORIGIN
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Series: IRKP Plate: 5 Row: 9 Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROD 07-AUG-2002
1256 GGGAAAACAGAGCTAAAACTACAAGAACACTGAACCAGTCCTGGACTCTGATGGTTCTTAC 1315
                                                                         1436 CCGGGTAAATGAGCTCAGCACCCACAAAACTCTCAGGTCCAAAGAGACACCCACACTCAT 1495
                                                                                                                                                                                                                                                                                                                                                                1398 TGCAACGTGAGACACGAGGGTCTGAAAATTACTACCTGAAGAAGACCATCTCCCGGTCT 1457
                                                                                                                                                                                                                                          1458 CCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCACCCAT 1517
                                                                                                                                                                                                                                                                                                                                          1518 ATCCATGCATCCTTGTATAAATAAAGCATCCAGCAAAGCCTGGTACCATGTAAAAAAA 1577
                                                 1338 TTCATATATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCTTCTCA 1397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniáta; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1593)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (03-DEC-2001) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus, Similar to immunoglobulin heavy chain 1 (sei
IgG2a), clone MGC:6529 IMAGE:2651493, mRNA, complete cds.
BC018535
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Contact: MGC help desk
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FINITION

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/translation="mgwswiflfrlsgtagylsevologosgpelvktgasykmsckas
gytfsdyymhwykoshgkslewigylypnnggngynokfkgkatltydkssstaymel
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SQSITCNVAHPASSTKVDKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVL
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MYTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFWYSKLRVEKKNWVERNSYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 CCCCTGGGTGTGGAGATACAACTGGTTCCTCCGTGACTCTGGGATGCCTGGTCAAGGGCT 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        553 ACTICCCIGAGICAGIGACIGIGACTIGGAACTCIGGAICCCIGICCAGCAGIGIGCACA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               613 CCTTCCCAGCTCTCCAGCTCTGGACTCTACACTATGAGCAGCTCAGTGACTGTCCCCT 672
                                                                                                                                                                                                                                                                                                                                          RSLTSEDSAVYYCARGYISYYSYDHYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 GAGACACAGACTATAATGCAGCTTTCATATCCAGACTGAGCATCAGCAAGGACAATTCCA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 GIGGTAAATGGCTACAACCAGAAGTICAAGGGCAAGGCCACATIGACTGTAGACAAGICCI 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 AGAGCCAACTCTTCTTTAAAATGAACAGTCTGCGAGCTACTGACACAGCCATATATTACT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 CCAGCACAGCCTACATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373 GIGCCAGAAATAGAGGGGATATITACTATGATITCACTTATGCCATGGACTACTGGGGTC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 GIGCAAGA---GGATATATAAGTTACTATAGTTACGATCACTACTTIGACTACTGGGGCC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 AAGGAACCTCAGTCACCGTCTCCTCAGCCAAAACAACCCCCCATCAGTCTATCCACTGG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      438 AAGGCACCACTATCACAGTCTCCTCAGCCAAAACAACAGCCCCATCGGTCTATCCACTGG 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 GCTGTGTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCAC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 AGAGCCIGICCAICACCIGCACAGICTCTCTGAITAACIAGCIAIGGIGIACACT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 GGGTTCGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGAGTGAT---GGAGTGGTG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201 GGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGATATATTTATCCTAACAATG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 CTTCAGTGAAGATGTCCTGCAAGGCTTCTGGATACACATTCAGTGACTACTACATGCACT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ACACACTGACTCTAACCATGGGATGGAGCTGGATCTTTCTCTTCCTCCTGTCAGGAACTG 80
                                                                                                                               /product="Similar to immunoglobulin heavy chain 1 (serum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 940.8; DB 10; Length 1593;
Pred. No. 9.5e-243;
0; Mismatches 342; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 t
                               /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                          /protein_id="AAH18535.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVVHEGLHNHHTTKSFSRTPGK"
                                                                                                                                                                                                                                              /db_xref="GI:17391266"
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/lab_host="DH10B"
                                                                                                       /codon_start=1
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76.8%;
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791	852 839	912 899	972 959	1032	1092 1079	1152 1139	1212 1199	1272 1259	1332	1392 1379	1452 1439	1512 1499	1572 1559		
	793 GCAAGGAGTGTCACAAATGCCCAGCTCCTAACCTCGAGGGTGGACCATCCGTCTTCATCT	853 TCCTCCAAATATCAAGGATGTACTCATGATCTCCCTGACACCCAAGGTCACGTGTGTGG 	913 TGGTGGATGTGAGCGAGGATGACCCAGACGTCCAGATCAGCTGGTTTGTGAACAACGTGG 	973 AAGTACACACAGACACAAACCCATAGAGGATTACAACAGTACTATCGGGTGG	1033 TCAGCACCCCCCCATCCAGCACCAGGACTGGATGGCAAGGAGTTCAAATGCAAGG	1093 TCAACAAGAAGACCTCCCATCACCCATCGAGAACCATCTCAAAAATTAAAGGGCTAG 	1153 TCAGAGCTCCACAAGTATACATCTTGCCGCCACCAGCAGAGCAGTGTCGTCCAGGAAAGATG 	1213 TCAGTCTCACTTGCCTGGTGTGGGGTTCAACCCTGGAGACATCAGTGTGGAGTGGACCAGAGTGTGTGT	1273 GCAATGGGCATACAGAGAGAACTACAAGGACACCGCACCAGTCCTGGACTCTGACGGTT 	1333 CTTACTTCAFATAGCAAGCTCAATATGAAAACAAGCAAGTGGGAGAAAACAGATTCCT 	1393 TCTCATGCAACGTGAGACTCTGAAAAATTACTACCTGAAGAAGACCATCTCCC	1453 GGTCTCCGGGTAAATGAGCTCAGCACCCACAAAGCTCTCAGGTCCTAAGAGACACTGGCA 	1513 CCCATATCCATGCATCCCTTGTATAAATAAAGCATCCAGCAAAGCCTGGTACCATGTAAA	1573 AAAAAAAAAAAAA 1588 	
qq	Qy Dp	go Op	ζζ. Op	2y . Ob	2 <u>y</u> 3b	2y 3b	λ <u>γ</u>	2y 3b	λy Jb	<i>yy</i>	2y do	ζζ Q(ły dv	ły ib	

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GTCCTATCCCAGGTGCAGCTGAAGCAGTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGC 140
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                                                                                                                                                                                                                                                                                                                                                                                         201 CGTCAGTCTCCAGGAAAGGGTCTGGAGTGGCTGGGA---GTGATATGGAGTGGTGGAGAC 257
                                                                                                                                                                                                                                                                                                                                                                                                          258 ACAGACTATAATGCAGCTTTCATAT¢CAGACTGAGCATCAGCAAGGACAATTCCAAGAGC 317
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                                                                                                                                                                                   CTCCATCAGAGCATGGCTGTCTTGGGGCTGCTCTTCTGCCTGGTGACATTCCCAAGCTGT
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                                                                                                                                                    Indels 36; Gaps
                                                                                                                    Length 1570;
                                                                                                                  Score 939.2; DB 6;
Pred. No. 2.6e-242;
0; Mismatches 323;
   12-JAN-1999;
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                  Location/Qualifiers
                                              /organism="unknown'
443 c 356 a
                                                                                                                    59.18;
77.18;
Patent: US 5859205-A
                                                                                                                                                 Matches 1209; Conservative
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                                                                                                                                 Similarity
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PAT 29-SEP-1999

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AR029102 1570 bp Sequence 6 from patent US 5859205.

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RO29102

AR029102.1 GI:5941075

1 (bases 1 to 1570)
Adair,J.Robert., Athwal,D.Singh. and Emtage,J.Spencer.
Humanised antibodies

Unclassified. Unknown. Unknown

ORGANISM

EFERENCE AUTHORS

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1016 GCCTCCCCATCCAGCACCAGGACTGGATGACTGGCAAGGAGTTCAAATGCAAGGTCAAC 1075
                                                                                                                                                                                                                                                             1098 AACAAAGACCTCCCATCACCATCGAGAGAACCATCTCAAAAATTAAAGGGCTAGTCAGA 1157
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                                                                                                                                                        1038 ACCCTCCCCATCCAGCACCAGGACTGGATGAGTGGCAAGGAGTTCAAATGCAAGGTCAAC 1097
896 GATGTGAGCGAGGATGACCCAGATGTCCAGATCAGCTGGTTTGTGAACAACGTGGAAGTA 955
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arch completed: June 23, 2003, 22:24:18 b time : 4285.96 secs

1556 AAAAAAAA 1563

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Q99131 mus musculu Q8r3v9 mus musculu Q991c4 mus musculu Q9r1a4 mus musculu Q8rc77 homo sapien Q8tc63 homo sapien
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0921k1 mus musculu
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Q8r3h6 mus musculu
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                                                                                   June 18, 2003, 16:41:53; Search time 67.8062 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Q8R3V9
Q99LC4
Q9R1A4
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Q921K1
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Gapop 10.0 , Gapext 0.5
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		1	091205; 01-DEC-7 01-DEC-3 01-JUN-7 HYPOThel	Mus m Eukar Mamma NCBI	[1] SEQUES Strau: Submit EMBL; MGD;]	nter nter fam;	PROSITE; PROSITE; Hypotheti	Match Local			
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                                                                                                                                                                                                                                                                   243 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLIPKVTCVVVDVSEDDP 302
                                                                                                                                                                                                                                                                                                            DVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSP 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 WLGVIWSG-GDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.7 kDa protein.
Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                        46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025447; AAH25447.1; -
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REQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;
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STRAIN-C57BL/63; TISSUE-PANCREAS;

MEDLINE-21085660; PubMed=11217851;

A RAWAN J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Gissi C., King B., Kochiwa H.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombeerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Parama M., Parama M., Rodriguez I., Sakamoto N.,

Parama M., P
                                               70 IWSG-GDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYA 128
365 RTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKD 424
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                                                                                                                                                                                                                                                            421 TAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 474
                                                                                                                                                                                                        425 TAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
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"Functional annotation of a full-length mouse cDNA collection.";
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SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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19, Last annotation update)
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InterPro; IPR003006; Ig_MHC.
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InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_c1.
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IGH-1 OR 1810060009RIK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wus musculus (Mouse)
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243 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDP 302
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InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_W.
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InterPro; IPR003599; Ig.
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                                                                185 SSGVHTFPALLQSGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPI-TQ 243
                                                                                                                  129 MDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFFESVTVTWNSGSL 188
             SSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTI 248
                                                                                                                                                     FVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTIS 368
                                                                                                     NPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISW 308
                                                                                                                                                                                                       369 KIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPV 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.4%; Score 1719.5; DB 11; Length 473;
68.6%; Pred. No. 3.2e-133;
ive 58; Mismatches 80; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                         429 LDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003888; AAH03888.1; -.
HSSP; P01842; 7FAB.
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SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;
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                                                                                                                                                                                                                                                                                                                                                     473 AA
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                                                                                                                                                                                                                                                                                                                                                     PRT;
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_like.
InterPro; IPR003596; Ig_MIC.
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SMART; SM00410; IG_like; 1.
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SMART; SM0409; IG; 2.
SMART; SM0407; IGc1; 3.
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245 P--TIKPCPPC----KCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPD 298
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                                                                                                                                                                                                                                                                                   244 PISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPD 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 ERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYK 423
184 NSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSG 243
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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EMBL; BC003878; AAH03878.1; -.
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
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PRELIMINARY;
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              239 GP--TIKPCPPC----KCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDP 292
                                                    303 DVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSP 362
                                                                    363 IERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENY 422
                                                                                                                                         70 I---WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 YAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187 SLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPIS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 SLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVP---- 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 TINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQI 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 --RDC-GCKPC-ICTVPEVS---SVFIFPPRKPKDVLTITLTPKVTCVVVDISKDDPEVQF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 SWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERT 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367 ISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLFSYGVHWVRQSPGKGLEWLGV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LVTLLNGIQCEVNLVESGGGLVQPGGSLRLSCAASGFTFTDYYMSWVRQPPGKALEWLGF 69
                                                                                                                                                                                           423 KDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                              Query Match 59.7%; Score 1523.5; DB 11; Length 469; Best Local Similarity 61.7%; Pred. No. 4.3e-117; Matches 291; Conservative 65; Mismatches 101; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024405; AAH24405.1; -.
Hypothetical protein.
SEQUENCE 469 AA, 51976 WW, 534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kDa protein.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
                                                                                                                                                                                                                                                                                                                   08R3V9
                                                                                                                                                                                                                                                                                ESULT 6
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77 TYYSEKFRGKATLTTDKSSSTAYMHLSSLTSEDSAVYFCARSS---YYSYD-LFAYWGQG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 TDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 TSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 ECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSY 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 VHSQVQLQQSGAELARPGASVRLSCKASGYTFTGYGVSWVKQTTGQGLEWVGEIYPGSGN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 VLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSG-GD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.7%; Score 1471.5; DB 11; Length 463;
60.3%; Pred. No. 8.1e-113;
tive 69; Mismatches 98; Indels 17; Gaps
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 436 FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 FIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHTEKSLSHSPGK 463
                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 463 AA; 51007 MM; EAA674C6BBC30783 CRC64;
                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGC1; 2.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; BC003435; AAH03435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:96446; Igh-4.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279; Conservative
PRELIMINARY:
                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01842; 7FAB
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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437 AA

PRT;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVKGRFTIYKDKDRNILSLQMSSLRSEDTAMYYCA--RGD-----YSA-YWGPGTLVTV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 PAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQT 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321 QTHREDYNSTIRVVSTLPIQHQDWASGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVY 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 ILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSK 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 VQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGDTDYNA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VOLOESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVASFSSGGIIYYTD 60
                                                                                                                                                                                                                                                                                                     Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rust monoclonal antibody (Mab 7, its light and heavy chains) and construction of a single chain antibody (scPV).";
Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFIS2372;
AAD40243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Gaps
                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 1456.5; DB 11; Length 437; 61.1%; Pred. No. 1.3e-111;
Live 62; Mismatches 95; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;
     01.MAY-2000 (TrEMBLrel. 13, Created)
01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 4.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:96446; Igh-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01842; 7FAB.
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                       NCBI_TaxID=10090;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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01-JUN-2002 (TrEMBLrel. 21, Created)

PRELIMINARY;

Q8TC77 Q8TC77

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RESULT 9

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122 --YYDFTYAMDYWGQGTSVTVSSAK†TPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 LEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 GLEWLGVIWSGGDTDYNAAFI-SRL$ISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 GLEWVSSMSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 VEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 EDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKD 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    359 LPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 EENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                 4 LGLLFC-LVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGK 62
                                                                                                                                                                                                                                                                                                                                                                                 3 LGLRWVFLVAILEGVQCEVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGK 62
                                                                                                                                                                                                                                                                            Suery Match 55.2%; Score 1409; DB 4; Length 471; Best Local Similarity 57.3%; Pred. No. 1.2e-107; Aatches 275; Conservative 74; Mismatches 115; Indels 16; Gaps
                                                                 Eukaryota; Metazoa; Chordata; Cranhata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                       Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC024289; AAH24289.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025985; AAH25985.1; -.
                                                                                                                                                                                                                                         471 AA; 51791 MW; 388F7F4CF588660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEOUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last apnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last adnotation update)
Hypothetical 52.0 kba protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                 Hypothetical 51.8 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                   Homo sapiens (Human)
                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                       TISSUE-SPLEEN;
                                                                                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                              SEQUENCE
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 Qγ
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 JTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDK 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 GDIYYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPES 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 KLEPS-GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 RVESKYGP-----PCP------SCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 VSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNN 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 KDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352 KGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNOVSLTCLVKGFYPSDIAVEWESNG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 HTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSP 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      412 OPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSL 471
                                                                                                                                                                                                                                                                                                                                                               59 SPGKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 PPGKGLEWIGTINFSGNMYYSPSLRSRVTMSADMSENSFYLKLDSVTAADTAVYYCA--A 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 GHLVMGFG---AHWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 VTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDK 237
                                                                                                                                                                                 1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSL--TSYGVHWVRQ 58
                                                                                                                                                                                                                                                                        8 MKHLWFFILLLVAAPRWVLSRLQLQESGPGLLKPSVTLSLTCTVSGDSVASSSYYWGWVRQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Organization of the equine immunoglobulin heavy chain constant region genes. III. Alignment of c-mu, c-gamma, c-epsilon and c-alpha genes."; Immunobiology 199:105-119(1998).
                                                                                           20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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Leibold W., Radbruch A.;
53.4%; Score 1362; DB 4; Length 4<sup>7</sup>55.6%; Pred. No. 8.7e-104;
Live 78; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Immunogobulin gamma 1 heavy chain constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 337 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AJ300675; CAC44624.1; -...
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98383416; PubMed-9717671;
                                                  Local Similarity 55.6%
hes 268; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (Horse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     477 GK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 GK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fradment).
         Query Match
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                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 IYYDFTYAMDYWCQGTSVTVSSAKTTPPSVYPLA-PGCGDTTGSSVTLGCLVKGYFPE-S 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 ---NYEGAMDYWGQGTSVTVSSEPAREPTIYPLTFPQA--LSSDPVIIGCLIHDYFPSGT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 VTVTW-NSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWP-SQTVTCSVAHPASSTTVD 236
                                                                                                                                                                                                                                                                          143 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S 201
                                                                                                                                                                                                                                               202 GLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCP 261
                                                                                                                                                                                                                                                                                                                                             262 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                            322 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNG--HTEENYKDTAPVLDSDGSYFIYS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46; Gaps
                                                                                                 5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                 DB 6; Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.9%; Score 941; DB 11; Length 482; 44.7%; Pred. No. 4.2e-69; . . tive 75; Mismatches 152; Indels 46
                                                 41.1%; Score 1049.5; DB 6; Length 58.4%; Pred. No. 2.9e-78; Live 54; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC011181; AAH11181.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN 2.
PROSITE; PS0290; IG_MHC; UNKNOWN 3.
PEQUENCE 482 AA; 51865 MW; 312E01F9C1BC7F3C CRC64;
337 AA; 37438 MW; A60BF2B01DEFD1F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            440 KLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown (protein for MGC:18822).
                                                                          58.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221; Conservative
                                                                                                   Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouerv Match
       SEQUENCE
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local
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us-09-770-916-2.rspt

01-JUN-2001 (TrEMBLrel. 17, Created)

61 GKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCAR--NR 118 177 ESVTVTW--NSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQT---VTCSVAHP-- 229 119 GDIYYDFTYAMDYWGQGTSVTVSSAK|TTPPSVYPLAPGCGDTTG--SSVTLGCLVKGYFP 176 180 DSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMQGTDEHVVCKVQHPNG 239 359 VPDQDTAIRVFAIPPSFASIFLIKST KLTCLVTDLTTYD-SVTISWTRQNGEAVKTHTN 416 240 NKEKNVPLPVIAELPPKVSVFVPPRDĢFFGNPRKSKLICQATGFSPRQIQVSWLREGKQV 299 300 GSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMC- 358 262 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNN---VEVHTA 318 474 DVYLLPPAREQLNLRESATITCLVTGFSPADVFVQMMQRGQPLSPEKYVTSAPMPEPQAP 533 319 QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGL-VRAP 377 378 QVYILPPPAEQLS-RKDVSLTCLVVGRNPGDISVEWTSNGH--TEENYKDTAPVLD--SD 432 1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60 Query Match 33.2%; Score 846.5; DB 4; Length 597; Best Local Similarity 34.6%; Pred. No. 3.5e-61; Matches 203; Conservative 88; Mismatches 180; Indels 115; Gaps Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 433 GSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478 TINPCP-----PCKECHK---InterPro; IPR003597; 19.
InterPro; IPR0035097; 19_c1.
InterPro; IPR003600; 1g_like.
InterPro; IPR003006; 1g_MHC.
InterPro; IPR003506; 1g_WHC.
InterPro; IPR003596; 1g_V.
InterPro; IPR00407; 1g; 5.
SWART; SW00409; 1G; 2.
SWART; SW00406; 1GV; 1.
SWART; SW00410; 1G_like; 1.
PROSITE; PS00290; 1G_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 597 AA; 65274 MW; 2DAFABFEDE055851 CRC64; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC002963; AAH02963.1; -01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Hypothetical 65.3 kDa protein. 230 ASSITVDK---KLEPSGPIS-----InterPro; IPR003599; Ig. HSSP; P01825; 7FAB. SEQUENCE FROM N.A. NCBI_TaxID=9606; Strausberg R.; TISSUE=LYMPH; DE DE BERNAR RESTANDE DE BERNAR RESTANDE BERNAR RESTANDER BERNAR RESTANDER BERNAR RESTANDER BERNAR RESTANDER BERNAR RESTANDER RESTANDER BERNAR g οp δλ δλ ò q qq ŏ Qγ g ò g g ğ δ

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61 GKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 SVTVTW--NSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQT----VTCSVAHP--- 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     230 -----A 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 KEKNVPLPVIAELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 SSTTVDK---KLEPSGPIS-----TINPCP-----PCKECHK------CPA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 SGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGLTFQQNASSMC-V 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNN---VEVHTAQ 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 TQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGL-VRAPQ 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      379 VYILPPPAEQLS-RKDVSLTCLVVGFNPGDISVEWTSNGH--TEENYKDTAPVLD--SDG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 IYYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAP---GCGDTTGSSVTLGCLVKGYFPE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.4%; Pred. No. 5.8e-61;
Matches 200; Conservative 93; Mismatches 171; Indels 118; Gaps
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC011857; AAH11857.1; -.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Igj 5.
SMART; SMO0408; IGc2; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 SYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 : | | : : | :::| | | | | ::|: :| 530 RYFAHSILTVSEEEWNTGETYTCVVAHEALPURVTERTVDKS 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain.
SEQUENCE 613 AA: 67273 MW; 31214203FB8421E7 CRC64;
                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:20337).
                                               PRT;
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SULT 15
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earch completed: June 18, 2003, 16:46:07 ob time: 70.8062 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 18, 2003, 16:41:52; Search time 19.4691 Seconds (without alignments) 1018.315 Million cell updates/sec Run on:

US-09-770-916-2 2552 Title:

Perfect score:

1 MAVLGLIFCLVTFPSCVLSQ.....RHEGLKNYYLKKTISRSPGK 478

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Potal number of hits satisfying chosen parameters:

Winimum DB seq length: 0 Waximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P01866 mus musculu	snm /	P01863 mus musculu	P01865 mus musculu	P01864 mus musculu	P20761 rattus norv	P20762 rattus norv	P22436 mus musculu	Snw	P01868 mus musculu	P01869 mus musculu	P20759 rattus norv	0	P01857 homo sapien	-	cavia	homo	homo	homod	mus m	P01819 mus musculu				P06336 mus musculu	P01854 homo sapien		P23084 heterodontu	P23087 heterodontu	P03988 oryctolagus	_	_	P23088 heterodontu
SUMMARIES	ID	GCB_MOUSE	GCBM_MOUSE	GCAA_MOUSE	GCAM_MOUSE	GCAB_MOUSE	GCB_RAT	GCC_RAT	GC3_MOUSE	GC3M_MOUSE	GC1_MOUSE	GCIM_MOUSE	GC1_RAT	GCA_RAT	GC1_HUMAN	GC_RABIT	GC2_CAVPO	GC2_HUMAN	GC4_HUMAN	GC3_HUMAN	HV45_MOUSE	HV43_MOUSE	HV44_MOUSE	MUC_HUMAN	EPC_RAT	EPC_MOUSE	EPC_HUMAN	HVC2_HETFR	HVC1_HETFR	HVCS_HETFR	MUC_RABIT	MUCB_HUMAN	HVC3_HETFR	HVCM_HETFR
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æ	Query Match	70.6	70.4	55.6	ω.		52.0	٠.	٠ س	س	45.1	4	<u>.</u>	ω.	7	42.3			41.3	٠				18.7			: :	17.3		ζ.	16.9	9	16.7	16.7
	Score	1802	1797	1419	1414	1385.5	1326.5	1202.5	1170	1159	1150	1145	1112	1100	1087	1080.5	1080.5	1059	1054.5	777.5	584	256	205		C.//#	4/4	4/3	442.5	437.5	435.5	432.5	429	426.5	425.5
	esult No.	П	C7 (m •	-7 " (Λ (، م	~ (30 (ָר כ	3;	Τ;	12	13	14	15	9 T	17	81.	57	50	7 6	77	57.	4 C	2 5	9 5	17	87.0	29	30	31	35	33

P04221 oryctolagus	P20768 suncus muri	P20758 gorilla gor	P20957 xenopus lae	P01877 homo sapien	P01822 mus musculu	P01876 homo sapien	P01878 mus musculu	P06337 mesocricetu	P01872 mus musculu	P01873 mus musculu	
MUCM_RABIT	MUC SUNMU	ALC1_GORGO	HV02_XENLA	ALC2_HUMAN	HV46_MQUSE	ALC1_HUMAN	ALC_MOUSE	MUC_ME\$AU	MUC_MOUSE	MUCM_MOUSE	
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479	457	353	135	340	137	353	344	54	155	116	
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16.6	16.3	15.8	15.6	15.2	15.0			•	•	14.2	
422.5 16.6 420 16.5						15.0	14.9	14.6	14.6		

ALIGNMENTS

336 AA.	ed) sequence update) annotation update)		Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.		Takahashi N., Obata M., Honjo T.;	gamma2b chain ge			er F.R.;	untranslated regions of the murine			Richards J., Blattner F.R.:	e constant reg				,	JSt-duplication divergence of gamma			atsunaga C., Yamamoto K.,		<pre>f mouse immunoglobulin G2b."; 1).</pre>	DF GAL-GALNAC DISACCHARIDE WHICH IS	BY HOMOLOGY WITH OTHER IG GAMMA	DENCE IS SHOWN.			
RESULT 1 GCB_MOUSE STANDARD; PRT; AC PO1866.	(Rel. 01, Creat (Rel. 01, Last (Rel. 40, Last		aiyota; metazoa; Chofdata; malia; Eutheria; Rodentia; I_TaxID=10090;	[1] SEQUENCE FROM N.A. (A ALLELE).	Med=6766534; Kataoka T.,	from newborn nouse DNA.";	Nature 283:786-789(1980). [2]	SEQUENCE FROM N.A. (MPC 11). MEDLINE-80081501: PubMed=117548:	Ε.		Science 206:1299-1303(1979).	SEQUENCE FROM N.A.		e for	<pre>ZD immunogiobulin heavy chain."; Science 206:1303-1306(1979).</pre>	[4]	SEQUENCE FROM N.A. (B ALLELE). MEDLINE=82173203; PubMed=6803173;	Ollo R., Rougeon F.;	.2a and gamma 2b chain genes.";	Nature 296:761-763(1982).	CARBOHYDRATE-LINKAGE SITE THR-105.	MEDLINE=94216359; PubMed=7512967; Kim H., Yamaquchi Y., Masuda K., Matsunaqa	Irimura T., Takahashi N., Kato K.,	J. Biol. Chem. 269:12345-12350(1994	-!- PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE MODIFIED WITH 2 STALTC ACTD RESTRIES	• •	-!- MISCELLANEOUS: THE A ALLELE SEQUENCE		InterPro; IPR003006; Ig_MHC. InterPro; IPR003597; Iq_c1.	
RES GCB ID AC	4444	888	388	RN RP	RA RA	RI	R R N	RP RX	RA	RT	R. N	RP	RA RA	E E	R.F.	RN	RY RX	RA	RT	RL N	R.	K K	RA Ed	RI.	ខ្លួ	88	888	D.K	DR DR	•

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HREDYNSTIRVVSTLPIQHQDWASGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVXIL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 PNLEGGPSVFIFPPNIKDVLMISLTPRVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
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                                                                                                                                                                                                                                                                                                                                                                       O-LINKED (GALNAC. . .).
REMOVED POST-TRANSLATIONALLY (PROBABLE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                        INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                             Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
                                                                                                                                                                          INTERCHAIN (WITH A LIGHT CHAIN).
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T -> A (IN B ALLELE).
N -> D (IN B ALLELE).
N -> I (IN B ALLELE).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
H -> T (IN REF. 2 AND 3).
H -> T (IN REF. 2 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1802; DB 1; L
Pred. No. 1.2e-120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         443 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2B chain C region, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.6%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36658 MW;
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 335-405 FROM N.A.
                                                                                                  PROSITE; PS00290; IG MHC; 1.
                    Pfam, PF00047; 1g; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 336; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 AA;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HREDYNGTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
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                                                                                                                                             -!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MENA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND SEGMENT OF MU CHAINS.
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                                                                                                                                                                                                                                                                                          -!- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-335 IS ASSUMED TO BE
                                                                                                                                                                                                                                                                                                           IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM.
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Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
                                                              Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 405;
                                                                                                     "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";
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Pred. No. 3.6e-120;
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                    MEDLINE=82115295; PubMed=6799207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44330 MW;
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100.0%;
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MGD; MGI:96445; Igh 3.
InterPro; IPR003060; Ig_MHC.
InterPro; IPR003597; Ig_Cl.
InterPro; IPR003600; Ig_like.
                                  SEQUENCE OF 335-378 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
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1118
150
256
352
370
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181 HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 240
                                                               383 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
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Ollo R., Auffray C., Morchamps C., Rougeon F.;
"Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
"The Complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
Nucleic Acids Res. 9:1365-1381(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sikorav J.-L., Auffray C., Rougeon F.; "Structure of the constant and 3' untranslated regions of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implications for the evolution of immunoglobulin structure and function.";
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               de Preval C., Fougereau M.; "Determination of the primary structure of a mouse gamma G2a immunoglobulin. Identification of the disulfide bridges."; Eur. J. Blochem. 30:452-462(1972),
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                                                                                                                                              301 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG 335
                                                                                                                     443 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG 477
                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Ig gamma-2A chain C region, A allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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DISULFIDE BONDS
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143 AKTTPPSVYPLAPGCGDTTGSSVTLĠCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
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"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.",
Proc. Natl. Acad. Sci. U.S., 79:2623-2627(1982).
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT TONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55.6%; Score | 1419; DB 1; Length 330; 78.6%; Pred. | No. 1.6e-93; Live 30; Mismatches 36; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                               REMOVED POST-TRANSLATIONALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36389 MW; B84361C5445A6864 CRC64;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, membrane-bound form.
                                                                                                                                                                                            Immunoglobulin domain; Immunoglobulin C region.
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                      IPR003597; Ig_c1.
IPR003600; Ig_like.
                                                                              Pfam; PF00047; ig; 2.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGcl; 2.
PROSITE; PS00290; IG_MHC; 1.
InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 AA;
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                            InterPro;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-i- MISCELLANDOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
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INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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4C38138BFAED3FF0 CRC64;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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399 AA;
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21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update)

STANDARD;

GCAB_MOUSE

CAB_MOUSE

P01864;

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                                                                                                                                                                                                                                                                                                                                      chain Fc regions of Igla and Iglb allotypic forms.";
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
                                                                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                      Dognin M.J., Lauwereys M., Strosberg A.D.; "Multiple amino acid substitutions between murine gamma 2a heavy
                                                                                                                                                                         Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.; "Multiple differences between the nucleic acid sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 AA; 36596 MW; FA3382792CBB13C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 VQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%; Score 1385.5; DB . 77.1%; Pred. No. 3.9e-91; tive 33; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain; Immunoglobulin C region.
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2A chain C region, B allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00479; -; NOT_ANNOTATED_CDS.
                                                                                                                                             STRAIN=C57BL/6;
MEDLINE=82037861; PubMed=6170065;
                                                                                                                                                                                                                                                                                      MEDLINE=8203777; PubMed=6794027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00410; IG_like; 1. SMART; SM00407; IGcl; 2.
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                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A02153; G2MSAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                             SEQUENCE FROM N.A.
                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259;
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InterPro; IPR003600; Ig_like.
Pfam; PF00047; ig; 2.
                        01-FEB-1991 (Rel. 17, Last s
15-JUL-1999 (Rel. 38, Last a
Ig gamma-2C chain C region.
                                                                                                                                                                                                                                                                                                                                                         EMBL, X07189; CAA30169.1; -. PIR; S00847; S00847. HSSP; P01842; 7FAB. InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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                                                                        Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 229; Conserv
                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE-PSGPISTINPCPPCKECHKCP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 APNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 MGPPTEQLTEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bruegeemann M.;
Broolution of the rat immunoglobulin gamma heavy-chain gene family.";
Gene 74:473-482(1988).
PIR; PS0018; PS0018.
                                                                                                                                              Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (WITH A LIGHT CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1326.5; DB 1; Length
; Pred. No. 5.8e-87;
34; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               442 NMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain; Immunoglobulin C region.
                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-2B chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                   MEDLINE=89232738; PubMed=3149946;
                                                                                                                                                                                                                                                                                          HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003500; Ig_like.
Pfam; PF00047; Iq; 3.
                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.0%;
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                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                      ; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                             NCBI_TaxID=10116;
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DISULFID

DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID SEQUENCE Query Match 329 AA.

STANDARD;

GCC_RAT

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297

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MEDLINE=88166903; PubMed=3127222;
Brueggemann M., Delmastro-Galfre P, Waldmann H., Calabi F.;
"Sequence of a rat immunoglobulin gamma 2c heavy chain constant region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988). 47.1%; Score 1202.5; DB 1; Length 329; INTERCHAIN (WITH A HEAVY CHAIN). INTERCHAIN (WITH A LIGHT CHAIN). ; Pred. No. 3.5e-78; 35; Mismatches 65; Indels 36571 MW; 5FCD7B7933850773 CRC64; PROSITE; PS00290; IG_MHC; 1. Immunoglobulin domain; Immunoglobulin C region. 01-FEB-1991 (Rel. 17, Created) 01-FEB-1991 (Rel. 17, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)

us-09-770-916-2.rsp

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TRANSMEM
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DOMAIN
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                                                                                                                                            GC3M_MOUSE
                                                                                                                             RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 TIPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLOSGLY 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 TMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPN 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR-----IPKPSTPPGSSCPPGN 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 LEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHR 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 EDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPP 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Gaps
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniatà; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                         MEDLINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Wels J.A., Word E.Y., Blattner F.R.; "Structural analysis of the murine 1gG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 66.2%; Pred. No. 7e-76; Conservative 33; Mismatches 74; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   329 AA; 36228 MW; F45827174182BAD6 CRC64;
                  294 VDTDSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK 329
443 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                              01-AUG-1991 (Rel. 19, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                Ig gamma-3 chain C region, secreted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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HINGE.
                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; J00451; -; NOT_ANNOTATED_CDS.
                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP, P01857; IFC1.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 19; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 3:2041-2046(1984).
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
223
327
                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B02156; G3MSC.
                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 221;
                                                                                                                   GC3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                           236 PREQMSKKKVSLICLVINFFSEALSVEWERNGELEQDYKNIPPILDSDGTYFLYSKLIVD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
The structure of the mouse immunoglobulin in gamma 3 membrane gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITINE-85027161; PubMed-6092053; MELS J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Wels J.A., Word E.Y., Blattner F.R.; Structural analysis of the murine 1gG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Transmembrane; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.4%; Score 1159; DB 1; Length 398;
66.0%; Pred. No. 5.3e-75;
Live 33; Mismatches 74; Indels 6
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E -> Q (IN REF. 2).
P -> F (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
19-gamma-3 chain C region, membrane-bound form.
                                                                                               445 TSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                296 TDSWLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 11:6775-6785(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA24767.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=84041483; PubMed=6314258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 328-398 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P01857; 1FC1.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_C1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 3:2041-2046(1984).
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Matches 219; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00451; AAB59655.1;
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
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398 AA;
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145 TIPPSVYPLAPGCGDTIGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLY 204
                                                                                                                                                                                                                    205 TMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPN 264
                                                                                                                                                                                                                                                              385 PAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMK 444
                                                                                                                                                                                                                                                                                      265 LEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHR 324
                                                                                                                                                                                                  EDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPP 384
             2 TTAPSUYPLUPGCSDISGSSVTLGCLUKGYFPEPUTVKWNYGALSSGVRIVSSVLQSGFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-80202559; PubMed=6059752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Saidman J.G., Peterlin B.M., Leder P., Honjo T.;
Ilmmunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
MEDLINE-80012837; Pubmed-113776;
Rogers J., Clarke P., Salser W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=80045036; Pubmed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE BONDS (MOPC 21),
MEDLINE=73008889; PubMed=5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Evolution of immunoglobulin subclasses. Primary structure of murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C)
                                                                                                                                                                                                                                                                                                                                445 TSKWEKTDSFSCNVRHEGLKNYYLKKTISRSP 476
                                                                                                                                                                                                                                                                                                                                                    296 TDSWLQGEIFTCSVVHEALHNHHTQKNLSRSP 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 6:3305-3321(1979),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (MYELOMA PROTEIN MOPC 21).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma-1 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Mus musculus (Mouse)
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Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
-!- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA SPECIES FOR IG GAWMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED IN SEPRARTE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-44 FROM N.A.
MEDLINE-8222190; PubMed-6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloning and complete nucleotide sequence of mouse immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-82115295; Pubmed-6799207;
Rogers J., Chol E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Alternative splicing; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Gene segments encoding transmembrane carboxyl termini of
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                                                                                                                                                                                                               Ig gamma-1 chain C region, membrane-bound form
                                                                                                                                           01-AUG-1991 (Rel. 19, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                 393 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 323-393 FROM N.A. MEDLINE-82197626; Pubmed-6804950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-80045036; PubMed-115593;
                                                                                                     21-JUL-1986 (Rel. 01, Created)
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003597; Ig_cl.
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                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma 1 chain gene.";
Cell 18:559-568(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                     GC1M_MOUSE
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1M_MOUSE
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143 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
                                                                                                                                                                                                                                                                                                      203 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 262
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                                                                                                                                                                                                                                                                                                                                                                       323 HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
                                                                                                                                                                                                                                                                                                                                                                                                                           383 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Evolution of the rat immunoglobulin gamma heavy-chain gene family."; Gene 74:473-482(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                       62; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
                                              INTERCHAIN (WITH A LIGHT CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                              Length 393;
                                                                                                                                                                    4CC88343B7A1CE27 CRC64;
                                                                                                                 N-LINKED (GLCNAC. . .).
                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                           44.9%; Score 1145; DB 1;
64.5%; Pred. No. 5.2e-74;
tive 45; Mismatches 62;
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01-FEB-1991 (Rel. 17, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
19 gamma-1 chain C region.
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HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.
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SMART; SM00407; IGc1; 2.
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143 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
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                                                                                                                                                                                                                                                                                                         61 LYTLTSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPR-----NGGDCKPC-ICTG 113
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                                                                                                                                                                                                                                                                                                                                                                   323 HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
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                                                                                                                                                                                                                                                  Gaps
                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
013BAB45EF49B9DA CRC64;
                                                                                                                                                                          ; Score 1112; DB 1; Length 326;
; Pred. No. 8.8e-72;
50; Mismatches 68; Indels 10;
                                            INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
INTERCHAIN (WITH A HEAVY CHAIN).
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35946 MW;
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Matches 208; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI TaxID=10116;
                                                                                01-FEB-1991 (Rel. 17, Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 gamma-2A chain C region.
Rattus norvegicus (Rat).
     322 AA.
                                               01-FEB-1991 (Rel. 17, Created)
STANDARD;
                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             I_TaxID=10116;
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"Evolution of the rat immunoglobulin gamma heavy-chain gene family."; MEDLINE=89232738; PubMed=3149946; Gene 74:473-482(1988). Brueggemann M.;

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EMBL; M13804; AAA41376.1; ALT_INIT. PIR; PS0019; PS0019.
HSSP; P01842; 7FAB.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_C1.

MEDLINE=71064025; PubMed=5530842;

SEQUENCE OF 136-329 (EU)

				2;	202	09	262	107	322	166	382	226	442	286		
Pfam; PF00047; ig; 2. SMART; SM00407; IGc1; 2. PROSITE; PS00299; IG_MHC; 1. Immunoglobulin domain; Immunoglobulin C region.		107 107 INTERCHAIN (WITH A HEAVY	D 242 300 D 172 172 N-LINKED (GLCNAC) (POTENTIAL). E 322 AA; 35186 MW; E8EA136A9DE01EDB CRC64;	Query Match 43.1%; Score 1100; DB 1; Length 322; Best Local Similarity 60.4%; Pred. No. 6.2e-71; Matches 203; Conservative 53; Mismatches 66; Indels 14; Gaps	AKTTPPSVYPLAPGCGDT	TALKSNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQSG	LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA	LYTITISSYTVPSSTWSSQAVTCNVAHPASSTKVDKKIVPRECNPCGC	PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT	TGSEVS-SVFIFPFRTKDVLTITLTPRVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHA	HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL	PEKQSNSTLRSVSELPIVHRDWLNGKFFKCKVNSGAFPAPIEKSISKPEGTPRGPQVYTM	PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN	APPKEEMTQSQVSITCMVKGFYPPDIKTEWKMNGQPQENYKNTPPTMDTDGSYFLYSKIN		7 VKKETWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK 322
Pfam; PSMART; PROSITE Immunog	DISULFID DISULFID DISULFID	DISULFID	DISULFID CARBOHYD SEQUENCE	Query Matcl Best Local Matches 20	143		203	61	263	108	323	167	383	227	443	287
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MEDLINE=71064024; PubMed=5489771; Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D., Waxdal M.J., Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. VII. Amino Ellison J.W., Berson B.J., Hood L.E.; "The nucleotide sequence of a human immunoglobulin C gammal gene."; Nucleic Acids Res. 10:4071-4079(1982). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo. acid sequence of heavy-chain cyanogen bromide fragments H1-H4."; Biochemistry 9:3161-3170(1970). 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Ig gamma-1 chain C region. 330 AA. SEQUENCE OF 1-135 (MYELOMA PROTEIN EU). MEDLINE=82274238; PubMed=6287432; STANDARD; Homo sapiens (Human). SEQUENCE FROM N.A. NCBI_TaxID=9606; GC1_HUMAN RESULT 14 GC1_HUMAN us-09-770-916-2.rsp

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-1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.8-A resolution."; Biochemistry 20:2361-2370(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- MISCELLANDOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS.
                  Edelman G.M.; "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dreker L., Schwarz J., Reichel W., Hilschmann N.;

*Rule of antibody structure. The primary structure of a monoclonal 1961 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

### Comparison of the protein of the disulfide bridges."

### Comparison of the protein of the disulfide bridges."

### Comparison of the products of the disulfide bridges."

#### Comparison of the products of the disulfide bridges."
                                                                                                                                                                                                                                                                                    Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.; "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgGl KOL, I.". Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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                                                                                                                                                                  monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                        "The covalent structure of a human gamma G-immunoglobulin. X.
                                                                                                                                   Ponstingl H., Hilschmann N.; The rule of antibody structure of a
                                                                                                                                                                                                                                                       SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
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MEDLINE-81208100; PubMed-7236608;
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PIR; A02146; GHHU.
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                                                                                                                  PubMed=826475;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
                                                                  Biochemistry 9:3171-3181(1970).
                                                                                                    SEQUENCE (MYELOMA PROTEIN NIE).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
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PDB; 1FC2; 15-JUL-92.
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143 AKTIPPSVYPLAPGCGDITGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQ-S 201
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                                                                         PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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INTERCHAIN (WITH HEAVY CHAIN).
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D -> E (IN G1M(NON-1) MARKER).
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HINGE.
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Pfam; PF00047; ig; 3.
SMART; SM00410; IG_like; 1.
SMART; SM00407; IGc1; 2.
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322 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 381
             382 LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKL 441
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Oryctolagus cuniculus (Rabbit). Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus, 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 323 AA. STANDARD; gamma chain C region. GC_RABIT P01870; RESULT 15 3C_RABIT

NCBI_TaxID=9986;

MEDLINE-84030930; PubMed-6313520; Bernstein K.E., Alexander C.B., Mage R.G.; "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant SEQUENCE FROM N.A. haplotype.

Pratt D.M., Mole L.E.; "Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin G of different allotype."; Biochem. J. 151:337-349(1975). [2] SEQUENCE OF 1-128. MEDLINE-76135469; PubMed=1243651; Immunogenetics 18:387-397(1983).

SEQUENCE OF 88-266 FROM N.A. MEDLINE-83299917; PubMed-6193512; Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.; Martens C.L., Hoose K.W., Steinmetz M., Hood L., Knight K.L.; Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain and identification of two genomic C gamma genes."; Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).

SEQUENCE OF 132-161.
MEDLINE=70110015; PubMed=5461106;
Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
"Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin G."; Biochem. J. 116:249-259(1970).

Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
(In) Killander J. (eds.); SEQUENCE OF 129-131 AND 155-322.

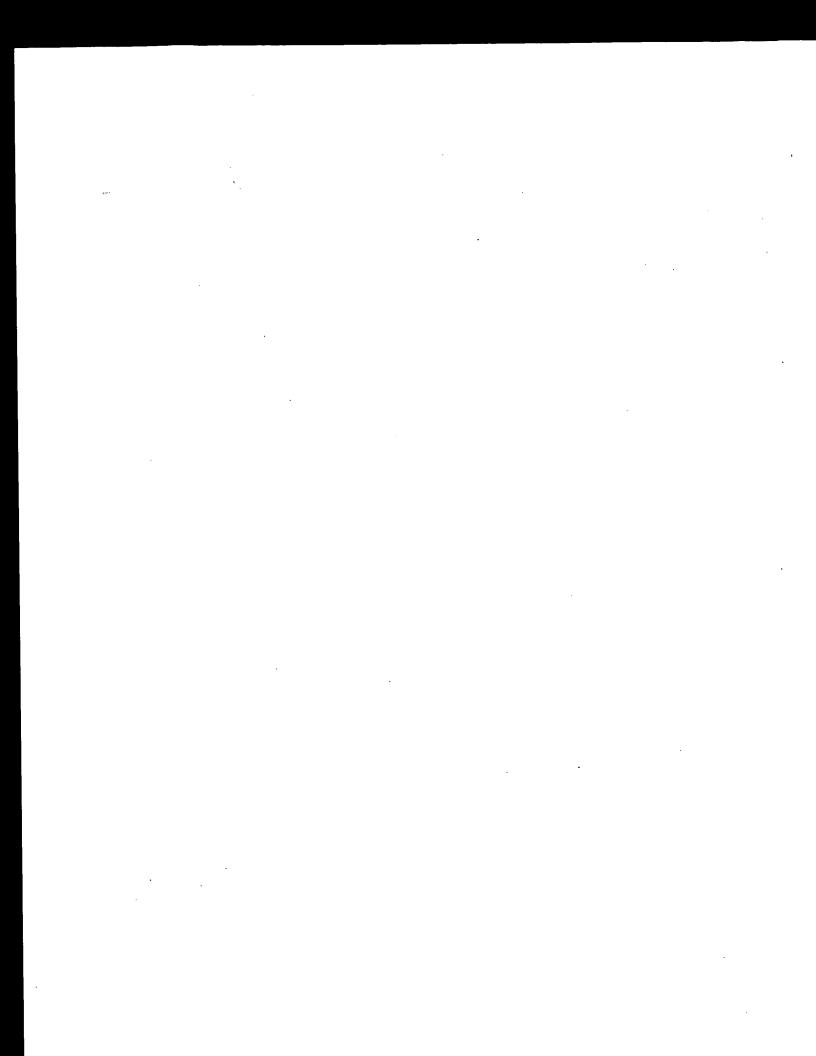
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell, Stockholm (1967)

Search completed: June 18, 2003, 16:42:31 Job time : 20.4691 secs

-!- MISCELLANEOÚS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER, 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15 MARKERS AND REF.5 THE E15 MARKER. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).

EMBL; M16426; AAA31289.1; -.

·	4,	206 65	264	324 169	384	444	
	Gaps	-SGLYTM :: SSGLYSL	CPAPN PTCPPPE	TQTHR PPLRE	YILPP : YTMGP	KLNMK	
	323;		ECHKCPAPN TCSKPTCPPPE	LEGGPSVFIFPPNIKDVLMISLTPKYTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHR 	EDYNSTIRVVSTLPIQHQDMMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPP : :	PAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENVKDTAPVLDSDGSYFIYSKLNMK : : ::	
	th s	/HTFPA : /RTFPS	CPPCKE	VNNVE	KIKGLV : KARGQP	SDGSG	
RKER). RKER). 2). 2). AND 4) AND 5) . (). (). (). (). (). (). (). (). ().	.,	SVYPLAPGCGDTTGSSVTLGCLVKGYRPESVTVTWNSGSLSSSVHTFPALLQ : :	SSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHK - - - - - - - - -	ICVVVDVSEDDPDVQISWFVNNV 	YNSTIRVVSTLPIQHODWMSGKEF ^K CKVNNKDLPSPIERTISK :	OTAPVI TPAVI	
85.000000000000000000000000000000000000	DB 1 -69; 62;	TWNSG TWNSG	PSGPI:	EDDPD' : : QDDPE'	LPSP11 : LPAP11	EENYKI : EDNYKI	478
BRANKER BERNAR C	re 1080.5; d. No. 1.5e Mismatches	ESVTV 	QTVTCSVAHPASSTTVDKKLEPS 	VVDVS	VNNKD : VHNKA	SNGHT KNGKA	SKWEKTDSFSCNVRHEGLKNYYLKTISKSPGK : :: : SEWQRGDVFTCSVMHEALHNHYTQKSISKSPGK
# 000000000000000000000000000000000000	0	KGYFE III I KGYLE	SSTTV	CVTCV	SPKCK IIII	VEWE	KKTIS :- : QKSIS
0g10bu	Score Pred. 8; Mis	SVTLGCLVKGY : TVTLGCLVKGY	TVTCSVAHPASS : ::	KDVLMISLTPKV - : KDTLMISRTPEV	WMSGKI : VLRGKI	APGDIS (PSDIS	CNYYL! : :
19_MHC. 19_C1. 2. MHC; 1. 11	38; 48;	GSSVT : SSTVT	TVTCS' : PVTCN	KDVLM 	ІОНОD! ТНОD!	LVVGF!	RHEGLI MHEALI
10. 19 10. 10. 19 10. 19 10. 19 10. 19 10. 19 10. 19 10. 19 10. 19 10	vat	CGDTT CGDTP	TWPSQ CSQ	FPPNI FPPKP	VSTLP VSTLP	VSLTCI VSLTCI	FSCNVF : : FTCSVN
HSSP; P01857, 1FC1. HSSP; P01857, 1FC1. InterPro; IPR003306; 1g_M InterPro; IPR003306; 1g_M Pfam; PF00047; 1g; 2. SMART; 2000407; 1Gc1; 2. SMASTIE; PS00290; IG_MHC; IMMUNOGILE; PS00290; IG_MHC; IMMUNOGILE; PS00290; IG_MHC; INTERNIT 184 184 VARIANT 184 184 VARIANT 185 185 CONFLICT 48 48 CONFLICT 173 173 CONFLICT 173 173 CONFLICT 201 201 CONFLICT 201 201 CONFLICT 256 256 CONFLICT 266 266 CONFLICT 266 266 CONFLICT 266 266 CONFLICT 260 260 CONFLICT 260 CONFLICT 260 CONFLICT 260 CONFLICT 260 CONFLICT 260 CO	Query Match Best Local Similarity 61. Matches 205; Conservative	PSVYPLAPG : PSVFPLAPC	SSSVTVPSS	GGPSVFIFPP 	STIRV	QLSRKDV8 : : ELSSRSV9	SKWEKTDSFSCNVRHEGLKNYYLKKIISRSPGK : :: : SEWQRGDVFTCSVMHEALHNHYTQKSISRSPGK
A02161; PO1857; Pro; IPR Pro; IPR Pro; O4040 ; SM0040 o41; Db111 o41; Db1111 o41; Db1111	Simil 5; C	PSVY : PSVF	SSSV - - SSVV	LEGG LLGG	EDYN : : QQFN	PAEQLS : PREELS	TSKW : TSEW
HSSP; P01 InterPro; InterPro; Pfam; PF0 SMART; SM PRART; SM PRART; SM NON TER VARIANT CONFLIC	Query Match Best Local (Matches 200	148	207	265	325	385	290
PIR; HSSP; HSSP; Interinterinterinterinterinterinterinteri	Query M Best Lo Matches						
DR D	OĂĬ	Qy Db	Qy	Qy Db	Qy Dp	Q _Y	Qy



GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

June 18, 2003, 16:41:57; Search time 34.9101 Seconds Run on:

(without alignments)
1316.302 Million cell updates/sec

US-09-770-916-2 Perfect score: ritle:

1 MAVLGLLFCLVTFPSCVLSQ.....RHEGLKNYXLKKTISRSPGK 478

sequence:

283224 seqs, 96134422 residues searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

otal number of hits satisfying chosen parameters:

finimum DB seq length: 0 faximum DB seq length: 20000000000

ost-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:* atabase :

pirl:* pir2:* pir3:*

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

S31459 S22080 G2MS11 G2MSBM PC4436 S37483 Query Match Length DB Score esult

Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-2a chain
Ig gamma-2a chain
Ig gamma-2a chain g gamma-3 chain C g gamma-3 chain C g gamma-1 chain C g gamma-1 chain C Ig gamma-1 chainIg heavy chain preIg gamma-2a chain
Ig gamma-2a chain
Ig gamma-2b chain
Ig gamma-2b chain
Ig gamma-3 chain
Ig gamma-3 chain
Ig gamma-1 chain
Ig gamma-2 chain
Ig gamma-3 chain
Ig gamma-4 chain
Ig gamma-2 chain
Ig gamma-2 chain
Ig gamma-3 chain
Ig gamma-3 chain
Ig gamma-3 chain
Ig gamma-2 chain gamma-3 chain C gamma-2 chain C gamma 2a chain heavy chain pre gamma-1 chain C gamma chain C r Description G2MSAM G2MSAB PS0018 S00847 G3MSC G3MSM G1MS G1MSM PS0017 PS0019 147159 G4HU S69339 I47160 G2GP A60764 A23511 GZMSA GHHO GHRB G2HU 1485.5 1456.5 1427.5 1419 1414 1385.5 1326.5 1202.5 1150 1145 1112 11100 1087 1080.5 1080.5 1072.5 1072.5 1059 1054.5 1054.5

A. Mccession: A26232.
A. Molecule type: DNA
A. Residues: 138-172, P',174-189, 'FP',193-376,'T',378-474 <TU2>
A. Molecule type: DNA
A. Residues: 138-172, P',174-189, 'FP',193-376,'T',378-474 <TU2>
B. Ollo, R.; Rougeon, F.
B. Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and g A. Reference number: A26233; MUID:82173203; PMID:6803173
A. Molecule type: DNA
A. Residues: 138-161, L', 163-189, 'FP', 193 300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OL A. Cross-references: GB:J00461
B. Kim, H.; Yannaquchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takah J. Biol. Chem. 269, 12345-12350, 1994

-2	Id epsilon chain C	Ta damma-2h chain	Ta gamma 3 chain o	ر ر	To damma 1 chain o	10	Ta damma chain	Id damma 4 chain c	Id heavy chain nre	To heavy chain (Ma	Id damma-1 chain C	Ta damma chain	To mi chain precur	To damma-3 house	To min chain - shee		
	538864	PC4155	147161	C30554	147158	S06611	838950	147162	S04845	868213	831866	PT0207	S14683	G3HUWI	S25705	B46529	
	7	7	7	7	7	7	7	7	7	7	4	7	~	÷	7	7	
	548	231	328	308	328	327	246	277	549	213	255	234	627	289	592	572	
	40.7	40.6	40.3	40.1	40.0	38.7	36.1	34.6	32.9	32.6	30.6	30.3	30.3	30.3	30.3	29.4	
	1039	1036	1028	1023.5	1022	987.5	921	884	840.5	831	781.5	774.5	774	772.5	772.5	751	
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

G2MS11	
Ig gamma-Zb chain - mouse	
C:Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text	2000
C.Accession: S25057; A02157; A26235; A26232; A26233; A53598	11-Dec-2000
R; Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F	.; Kreuzaler, F.
Submitted to the EMBL Data Library, July 1992	
A.) Description of a Tobacco mosaic virus (TMV) inactivating neotop specifi	ating neotop specifi
A)Accession: S25057	
A; Status: preliminary	
A; Molecule type: mRNA	
A) RESIDES: 1-4/4 < FISH	
Actions—Telefores: EMBL:X6/ZIU; NID:954826; PIDN:CAA47649.1; PID:954827	:g54827
nitammaki-hataoka, I.; Kataoka, T.; Takanashi, N.; Obata, M.; Honjo, Nature 283, 786-789, 1980	njo, T.
A) Title: Complete nucleotide sequence of immunoalohulin gamma2h chain gang glongs from	hain gone oloned fro
A; Reference number: A02157; MUID: 80120716; PMID: 6766534	marii gene croned 110
A;Contents: a allele	
A;Accession: A02157	_
A; Molecule type: DNA	
A; Residues: 138-161, 'L', 163-189, 'FP', 193-474 <yam></yam>	
A;Cross-references: GB:J00461	
A; Note: the sequence was determined from the germline gene	
R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.	
Science 206, 1299-1303, 1979	
A; Title: Structure of the constant and 3/ untranslated regions of the murine gamma2b	the murine gamma2b
A; Reference number: A26235; MUID:80081501; PMID:117548	
A; Contents: MPC 11	
A: MOJ POUT DE TYDE - MEND	
A; Residues: 138-172, P', 174-189, 'FP', 193-376, 'T', 378-474 <tii></tii>	
A; Note: Lys-474 is probably removed posttranslationally	
R; Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner,	F.R.
Science 206, 1303-1306, 1979	
A, Title: Sequence of the cloned gene for the constant region of murine gamma2b immuno	urine gamma2b immuno
A; Reference number: A26232; MUID:80081502; PMID:117549)

5

Gaps

5,

47: Indels

DB 2; Length 475;

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376 APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSY 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 PALLÓSGLYTMSSSYTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCPPCK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 TDYNAAFISKLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 SYFNEKFKGKATLIVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQVGLLPF----GYWGQG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 ECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEV 315
                                                                                                                                                                                                                                                                                                                              17 VLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSG-GD 75
                                                                                                                                                                                                                                                                                                                                                                  A; Note: this sequence was determined from the differentiated gene
                                 C; Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                          F.1-19/Domain: signal sequence #status predicted <SIG>F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>F:159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                          Query Match 79.3%; Score 2024.5; DB 2 Best Local Similarity 82.3%; Pred. No. 4.2e-115; Matches 381; Conservative 30; Mismatches 47;
                                                                     C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: C02154
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                                                                                                                                                                                                                                                                          Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapt in disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la Superfamily: immunoglobulin c region; immunoglobulin homology Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152/Disulfide bonds: interchain (to light chain) #status predicted
164-220,288-348,394-452/Disulfide bonds: #status predicted
247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
324/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 SQALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 TDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 TKFNEKFKGKATLTSDKSSNTAYMELSSLTSEDSAVYYCARD----YDYDW-FAYWGQG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 TSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF: 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 KECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVE 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 VHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLV 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 RAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 VHSEVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKPGQGLEWIGYINPNKDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 VLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGD- 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                  Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.0%; Score 2067; DB 1; Length 474; Best Local Similarity 83.8%; Pred. No. 1.1e-117; Matches 389; Conservative 29; Mismatches 38; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 YFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference number: A53598; MUID:94216359; PMID:7512967
Accession: A53598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                281-350/Domain: immunoglobulin homology <IM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387-454/Domain: immunoglobulin homology <IM3>
                                                                                                                                     Molecule type: profein
Residues: 234-251 <KIM>
Comment: The a allele sequence is shown.
                                                                                                                                                                                                                                                           Introns: 138/1; 236/1; 258/1; 368/1
                                                                                                                                                                                                                                                                                                                                                                                                                                           236-257/Region: hinge
                                                                                                             Status: preliminary
```

```
A; Molecule type: DNA
A; Residues: 335-405 < YAM>
A; Cross-references: GB:J00462
B; Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wa
CB:L 26, 1937, 1981
A; Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamm
A; Reference number: A02158; MUID:82115295; PMID:6799207
                                                                                                                                                         R;Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A;Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglo
A;Reference number: A02154; MUID:82222190; PMID:6283537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 335-378 <ROG>
A;Note: the translation of the first exon of the membrane-bound segment is given
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
                                             C;Species: Mus musculus (house mouse)
C;Date: 17-Dec-1982 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: C02154; A02158; B02157
Ig gamma-2b chain C region, membrane-bound form - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A02158
```

A; Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned fro

A; Reference number: A02157; MUID: 80120716; PMID: 6766534

A; Contents: a allele. A; Molecule type: DNA

de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W. Ir. J. Blochem. 176, 287-295, 1988 Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed Reference number: S01320; MUTD:88329081; PMID:3138116

:Cross-references: EMBL:X13188; NID:951780; PIDN:CAA31580.1; PID:951781

Molecule type: mRNA Residues: 1-475 <DE1>

Accession: S01321

Species: Mus musculus (house mouse)
Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999

gamma-2b chain precursor - mouse

SULT 2

Accession: S01321

A; Accession: B0215;

sn) (covalent) #status experimental

F;297/Binding site: carbohydrate (As 1-334 was assumed to be identical with the correspon go contain two mRNA species for Ig gamma chains. The matched in separate exons, that is homologous with matched 323. Consequenting e.e.	ar Qy 20 1a Db 1 bu Qy 79	Application		240 QY 379	OY 439 SKLNMKIPSKWEKTDSFSCOVYRH I	RESULT 5 S37483 Ig gamma-2a chain - mouse C;Species: Mus musculus (house mou	C;Dāte: 06-Jan-1995 #sequ C;Accession: 337483 R;Ducancel, F.F.D. submitted to the EMBL Data A;Reference number: 537483 A;Reference number: 537483 A;Accession: 537483 A;Accession: 537483 A;Accession: 537483 A;Beatus: preliminary A;Molecule type: mRNA A;Reaidus: 1-465 vDUC. A;Cross-references: EMBL:: C;Superfamily: immunoglobuli, E;276-345/Domain: immunoglobuli	Query Mat Best Loca Matches Qy Db	08 qq
35,'K' <ya2> sequence of residue lines producing Ic an alternative 3'</ya2>	1/1; 98/1; 120/1; 230/1; 335/1; 378, An immunoglobulin heterotetramer suite bonds. In some cases, such as In 1/1; immunoglobulin C region; immunos: alternative splicing; duplication; comain: immunoglobulin homology								

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KMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                                                                            TTGS$VTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 198
                                                                                                                                                                                                                                                             QTVT¢SVAHPASSTTVDKKLEPSGPISTINPCPPCKECH 258
                                                                                                                                                                                                                                                                            DVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318
                                                                                                                                                                                                                                                                                                                                                                                         QHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378
                                                                                                                                                                                                                                                                                                                                                                                                          SCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVGFWPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSG-GDTDY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIVSGFSLISYGVHWVRQSPGKGLEWLGVIW-SGGDIDY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    se) |
sion 06-Jan-1995 #text_change 23-Jul-1999
Score 1739; DB 2; Length 446;
2red. No. 6.8e-98;
Mismatches 66; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D:9406252; PIDN:CAA49868.1; PID:9406253 ton; |immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 core 1727.5; DB 2; Length 469;
red. No. 3.6e-97;
Mismatches 69; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||| |:: |: ||:||
|HEGLHNHHTTKSFSRTPG 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEGLKNYYLKKTISRSPG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mology <IMM>
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66 WLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 PISTINPCP-PCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 IERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNG--HTEE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 WLGGSGYDEDIDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCARVDYDSSHAF 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 SGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 -----CPDPCKHC-RCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 DVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 TYA-MDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 LLFVL-SAPRGVLSQVRLQESGPSLATLLQTLSVTCTISGFSLNNYGVDWVRQAPGKALE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 NYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
                                                                                                                                                            Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: S1459
R;Patri, S.; Nau, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Reywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Mismatches 115; Indels
57.1%; Score 1456.5; DB : 59.2%; Pred. No. 8.4e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Accession: S22080; S06610; A31303
R.Sanders, P.G.
submitted to the EMBL Data Library, November 1991
                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;277-346/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: X69797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S22080
A;Accession: S22080
                                                                                                                                                                                                                                                                                                                                     A; Reference number: S31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-472 <PAT>
                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                              A; Accession: S31459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                RESULT 7
                              qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: PC4436
Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A. Lochem. Biophys. Res. Commun. 240, 566-572, 1997
Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyr. Reference number: JC5810; MUID:98063277; PMID:9398605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Residues: 1-444 <AKA>
Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
                              196 PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 PAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVP-----RDC-GCK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSY 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318
                                                                                                                                         319 QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378
                                                                                                                                                                                                                                                                                                                                     379 VYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 AAFI----SRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEV 315
     199 LQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGDTDYN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Mus musculus (house mouse)
Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94; Indels 23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251-320/Domain: immunoglobulin homology <IMM>
22/Disulfide bonds: interchain (to 98) #status predicted
99/Disulfide bonds: interchain (to 109) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           onoclonal antibody 13-1 heavy chain - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.2%; Score 1485.5; DB 60.9%; Pred. No. 1.4e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282; Conservative 64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: protein
Residues: 1-444 <AKA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: PC4436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCOLT 6
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7;

Gaps

15;

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Ajintrons: 1/1; 98/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM; the subunits associate into C;Superfamily: immunoglobulin c region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
                                                                                                                                                                                                                                                                                                                                                A;Note: the sequence was determined from the germline gene R;Ollo, R.; Auffray, C.; Morchamps, C.; Rougeon, F. Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981
A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amin A,Reference number: A32659; MUID:74175517; PMID:4831970
A;Contents: annotation; myeloma protein MOPC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Note: this is one paper in a series reporting the sequence, for additional reference. A, Note: this sequence differs from that shown at a number of positions
            R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: A32657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. A,Reference number: A32660; MUID:73056887; PMID:4565406
A,Contents: annotation; MOPC 173, disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AKTIPPSVYPLAPGCGDITGSSVTLGCLVKGYFPESVTVTWNSGSLS$SVHTFPALLQSG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 PNLEGGPSVFIFPPNIKDVIMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323 HREDYNSTIRVVSTLPIQHQDWMSGKFFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        383 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F:98-113/Region: hinge
F:137-206/Domain: immunoglobulin homology <IM2>
F:137-210/Domain: immunoglobulin homology <IM3>
F:243-310/Domain: immunoglobulin homology <IM3>
F:15/Disulfide bonds: interchain (to light chain) #status experimental
F:27-82,144-204,250-308/Disulfide bonds: #status experimental
F:107,110,112/Disulfide bonds: interchain (to heavy chain) #status exper
F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.6%; Score 1419; DB 1; Length 33
78.6%; Pred. No. 1e-78;
tive 30; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the germline gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A32658; MUID:81223894; PMID:6787604
A; Accession: A32658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 VEKKNWVERNSYSCSVVHEGLHNHHTHKSFSRTPGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-330 < COLL>
A; Note: the sequence was determined from the ge
Note: Lys-330 is removed posttranslationally
R; Bourgois, A.; Fougereau, M.; Rocca-Serra, J.
Eur. J. Blochem. 43, 423-435, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;de Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
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                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:J00470
                                                                                                                                                                                                                                                                    A; Residues: 1-330 <YAM>
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                                                                                                                                                                                                                             A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                  R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g gamma-2a chain C region, secreted form (allele a) - mouse;

Species: Mus musculus (house mouse);

Species: Mus musculus (house mouse);

Date: 30-Sep-1980 #sequence_revision 01-Sep-1981 #text_change 16-Jun-2000;

Accession: A02152, A32658;

A32657; A32658;

Accession: A02152, A32659;

Hotleic Acids Res. 8, 3143-3155, 1980;

Hotle: Structure of the constant and 3' untranslated regions of the murine Balb/C gamma in the structure of the constant and 3' untranslated regions of the murine Balb/C gamma in the structure of the constant and 3' untranslated regions of the murine Balb/C gamma in the structure of the constant and 3' untranslated regions of the murine Balb/C gamma in the structure of the constant and 3' untranslated regions of the murine Balb/C gamma in the structure of the constant and 3' untranslated regions of the murine Balb/C gamma in the structure of the constant and 3' untranslated regions of the murine Balb/C gamma in the structure of the constant and a' untranslated regions of the murine Balb/C gamma in the structure of the constant and a' untranslated regions of the murine Balb/C gamma in the structure of the constant and a' untranslated regions of the murine Balb/C gamma in the structure of the constant and a' untranslated regions of the murine Balb/C gamma in the structure of the constant and a' untranslated regions of the murine Balb/C gamma in the structure of the structure of the constant and a' untranslated regions of the murine Balb/C gamma in the structure of the structu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 TYA-----MDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPES 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 VTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 KLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 SEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288 GHDDPEVKFSWFVDDVEVNTATTKPREEQFNSTYRVVSALRIQHQDWTGGKEFKCKVHNE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 DLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNG- 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -HTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFVL-SAPIGVLSQVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein F;161-225/Domain: immunoglobulin homology <IMM>F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Cross-references: GB:V00798; NID:951835; PIDN:CAA24178.1; PID:91333984
A;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109; Indels
                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross.references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
                                                                                                                                                         A; Reference number: S06610; MUID: 90097956; PMID: 2513487
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59.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Ig CH gamma-1
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                                                                                                                                                                                                            A; Accession: S06610
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6; Gaps

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A;Molecule type: protein
A;Residues: 118-267, "F', 269-328, 'G', 330-334 < DOG>
A;Residues: 118-267, "F', 269-328, 'G', 330-334 < DOG>
C;Comment: Lys'-35 is removed posttranslationally.
C;Comment: The sequence differs from that of the a allele, from BALB/C mice, at 15% o C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (C;Complex: An immunoglobulin peterotetramer subunit and IgM, the subunits associate into C;Superfamilly: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribognin, M.J.; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A;Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc reg
A;Reference number: A32656; MUID:82037777; PMID:6794027
A;Accession: A32656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl F; 20-84/Domain: immunoglobulin homology <IMl>
                                                                                                                                                                                                                       R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, D. Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981
A;Title: Multiple differences between the nucleic acid sequences of the IgG2a(a) and A;Reference number: A02153; MUID:82037861; PMID:6170065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           203 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-2b chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999
                                                                                             C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C;Accession: A02153; A32656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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F;248-315/Domain: immunoglobulin homology <IM3>
F;248-315/Domain: immunoglobulin homology <IM3>
F;15/Disulfide bonds: interchain (to light chain) #status predicted
F;27-82,149-209,255-313/Disulfide bonds: #status predicted
F;108,117/Disulfide bonds: interchain (to heavy chain) #status predicted
F;185/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 335;
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                                                            Ig gamma-2a chain C region, secreted form (allele b) - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain C57BL/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259; Conservative
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A; Residues: 1-335 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A02153
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: DNA
Residues: 1-329, K < YAZ>
Residues: 1-329, K < YAZ>
1. Immunol. 26, 819-826, 1989
2. Title: Sequence and polyadenylation site determination of the murine immunoglobulin ga
Reference number: 157809; MUID:90097953; PMID:2513486
Accession: 157809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
ncleic Acids Res. 9, 1365-1381, 1981
Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and evo
Reference number: A32657; WUID:81198976; PMID:6262729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
Comment: The sequence of residues 1-328 was assumed to be identical with the correspon
Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The matit it contains an alternative 3' end, encoded in separate exons, that is homologous wit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la superfamily: immunoglobulin C region; immunoglobulin homology Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
                                                                 Species: Mus musculus (house mouse)
Date: 19-Feb-1984 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
Accession: A02154; B32657; I57809
Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
oc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobul Reference number: A02154; MUID:8222190; PMID:6283537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 LYTLSSSVTVISSTWPSQSITCNVAHPASSTKVDKKIEPRGP--TIKPCPPC----KCPA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 PNLEGGPSVFIFPPNIKDVLAISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 PNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 PPPEEEMTKRQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.4%; Score 1414; DB 1; Length 399; 78.5%; Pred. No. 2.6e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: the sequence was determined from the germline gene
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                                        gamma-2a chain C region, membrane-bound form - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 VEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           137-206/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 329-399 <YAM>
Cross-references: GB:J00471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecule type: DNA
Residues: 373-399 <RES>
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                                                                                                                                                                                                                                                                                                                                                                 Accession: A02154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: B32657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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F;136-205/Domain: immunoglobulin homology <IM2>F;242-309/Domain: immunoglobulin homology <IM3> Best Local Similarity 66.2%; Matches 221; Conservative A; Cross-references: GB:J00451 A; Residues: 1-329 <WEL> F;97-112/Region: hinge DNA C; Accession: B02156 A; Molecule type: Query Match C; Genetics: qq δy g δy q qq δy a δ δ g g Dp ò ò δλ g δ g A;Residues: 1-333 CBNU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Rroc. Natl. Acad. Sci. U. S.A. 83, 6075-6079; 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibod A;Reference number: A25941; MUID:86287397; PMID:3016742 Sur. J. Immunol. 18, 317-319, 1988
7. Tyfile: Sequence of a rat immunoglobulin gamma-2c heavy chain constant region cDNA: ext
8. Reference number: S00847; MUID:88166903; PMID:3127222
8. Accession: S00847 143 AKTIPPSVYPLAPGCGDTIGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202 203 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE-PSGPISTINPCPPCKECHKCP 261 262 APNLEGGPSVFIFPPNIKDVLAISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQ 321 322 THREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYI 381 LPPPAEQLSRKDVSLTCLVVGFNPGDISVEWISNGHTEENYKDTAPVLDSDGSYFIYSKL 441 R.Brueggemann, M. Gene 74, 473-482, 1988 A.Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family. A.Reference number: PS0017; MUID:89232738; PMID:3149946 Species: Rattus norvėgicus (Norway řat) S.Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999 5; Gaps Cross-references: EMBL:X07189; NID:957602; PIDN:CAA30169.1; PID:9663228 Gaps 52.0%; Score 1326.5; DB 2; Length 333; 73.6%; Pred. No. 4e-73; DB 2; Length 329; K; Brueggemann, M.; Delmastro-Galfre, P.; Waldmann, H.; Calabi, F. ;Superfamily: immunoglobulin C region; immunoglobulin homology ; Pred. No. 4e-73; 34; Mismatches 50; Indels Indels 442 NMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478 47.18; Score 1202.5; DB 2; 68.28; Pred. No. 1.2e-65; F; 20-82/Domain: immunoglobulin homology <IMM> 20-84/Domain: immunoglobulin homology <IMM> Ig gamma-2c chain C region - rat (fragment) Best Local Similarity (3.00 Matches 248; Conservative Matches 229; Conservative A; Introns: 96/1; 117/1; 227/1 C; Accession: PS0018; B25941 C; Keywords: immunoglobulin Keywords: immunoglobulin A; Molecule type: DNA A; Residues: 227-333 <BR2> Best Local Similarity Residues: 1-329 <BRU> A; Status: preliminary A; Molecule type: DNA ; Molecule type: mRNA A; Accession: PS0018 A; Accession: B25941 ; Accession: S00847 Query Match C; Genetics: RESULT 13 a δλ පි à g à g à

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R;Wels, J.A.; Word, C.J.; Rimm, D.; Der Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Bl EMBO J. 3, 2041-2046, 1984
A;Title: Structure analysis of the murine IgG3 constant region gene.
A;Reference number: A02156; MUID:85027161; PMID:6092053
A;Accession: B02156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aintrons: 97/1; 113/1; 223/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds: In some cases, such as 184 and 198, the subunits associate into c;Superfamily: immunoglobulin c region; immunoglobulin homology c;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogl
143 AKTTPPSVYPLAPGCGDTTGSSVTL¢CLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
                                                                                                                      203 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 262
                                                                                                                                                              61 LYTLSSSVTVPSSTWSSQTVTCSVAHPATKSNLIKKIEPRRP----KPRPPTDIC-SCD- 114
                                                                                                                                                                                                                                          263 PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT 322
                                                                                                                                                                                                                                                                         323 HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
                                                                                                                                                                                                                                                                                                                                                                                            383 PPPAEQLSRKDVSLTCLVVGFNPGDĮSVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig gamma-3 chain C region, secreted form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Mar_1987 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: the sequence was determined from the germline gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 VDTDSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK 329
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66.2%; Pred. No. 1.1e-63;
tive 33; Mismatches 74;
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Search completed: June 18, 2003, 16:47:04 Job time: 35.9101 secs
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Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobule 33/Domain: immunoglobulin homology <IM1>
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Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Blatt Bno J. 3, 2041-2046, 1984
Title: Structure analysis of the murine 1g63 constant region gene.
Reference number: A02156; MUID:85027161; PMID:6092053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: the sequence was determined from the germline gene Komaromy, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wall, R. icleic Acids Res. II, 6775-6785, 1983
Title: The structure of the mouse immunoglobulin in gamma-3 membrane gene segment. Reference number: A02155; MUID:84041483; PMID:6314258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 PAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMK 444
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                                  236 PREQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVD 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 IMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPAPN 264
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Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
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363-398/Domain: intracellular #status predicted <INT>
179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 45.4%; Score 1159; DB 1; Length 398; Best Local Similarity 66.0%; Pred. No. 6.4e-63; Matches 219; Conservative 33; Mismatches 74; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecule type: DNA
Residues: 328-332, 'G', 334-341, 'Q', 343-387, 'F', 389-398 <KOM>
Cross-references: GB:K00688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: the sequence was determined from the germline gene
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                                                                                                             445 TSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                     296 TDSWLQGEIFTCSVVHEALHNHHTQKNLSRSPGK 329
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   Molecule type: DNA
Residues: 1-398 <WEL>
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June 18, 2003, 16:41:57; Search time 56.3933 Seconds (without alignments) 2164.388 Million cell updates/sec
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Sequence 72, Appl
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                                                                                                                                                                 1 MAVLGLLFCLVTFPSCVLSQ.....RHEGLKNYYLKKTISRSPGK 478
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/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-429-660-10
PCT-USO2-02373-12
US-09-618-380A-7
PCT-USO2-34420A-23
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US-10-281-479A-23
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US-10-384-933-9
US-10-275-899A-82
PCT-USO2-36107-14
US-10-292-088-14
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US-10-292-088-70
PCT-USO2-36107-22
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US-10-292-088-30
PCT-US03-13054-4
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PCT-US03-10154-72
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                                                     OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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61 GKGLEWLGVIWSGGDTDYNAAFISRĻSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGD 120

9 9

1 MAVLGLLFCLVTFPSCVLSQVQLKQ\$GPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP

65.3%; Score 1666.5; DB 6; Length 469; 66.2%; Pred. No. 1e-99; Indels 11; Gaps

Best_Local Similarity 66.23 Matches 317; Conservative

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Query Match

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360 PSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTE 419

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Sequence 12, Sequence 12, Sequence 19, Sequence 38, Sequence 38, Sequence 57, Sequence 52, Sequence 62, Sequence 54, Sequence 54, Sequence 64, Sequence 66, Sequence 26, Seque	-78 Sequence 78, Sequence 78, Acid Delivery
PCT - US 02 - 36226 - 12 0S - 10 - 291 - 532 - 12 US - 10 - 291 - 532 - 12 PCT - US 31 - 10 + 9 + 8 US - 10 - 408 - 901 - 38 PCT - US 02 - 27220 - 5 US - 10 - 272 - 894 - 25 US - 10 - 272 - 894 - 25 US - 10 - 272 - 898 - 22 US - 10 - 292 - 088 - 54 US - 10 - 293 - 203	PCT-US02-36107 US-10-292-088- ALIGNMENTS 18 FOr Nucleic 710/429,662
	PCT-US US-10- 0429662 10ns For US/10/42' 5-02
44669 0 4465 0 4466 0 4	S S
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	27 55.9 470 2-10 0, Application US, FORMATION: Sandhu, Jasbir INVENTION: Compos, RENNE: 237.00001 PPLICATION NUMBER ILING DATE: 2003 SEQ ID NOS: 12 Patentin version 10 10 469 469 1: Homo sapiens 2-10
1445 1435.5 1435.5 1435.5 1435.1 1431.1 1431.1 1420.5 1429.1 1420.1 1420.1 1420.1 1420.1 1420.1 1420.1 1420.1 1420.1	RESULT 1 US-10-429-662-10 Sequence 10, Application US/ GENERAL INFORMATION: APPLICANT: Sandhu, Jasbir TITLE OF INVENTION: CURRENT APPLICATION COMPOSI; CURRENT APPLICATION NUMBER: CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2003- NUMBER OF SEQ ID NOS: 12 SOFTWARE: PATENTIN VETSION SEQ ID NO 10 LENGTH: 469 TYPE: PRT ORGANISM: HOME Sapiens
	RESULT 1 US-10-42 Sequen Sequen Sequen APPLIL TITLE TITLE CURRE CURRE CURRE NUMBE SOFTW SEQ IDD SEQ IDD SEQ ID SEQ

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61 GKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 DDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDL 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%; Score 1666.5; DB 6; Length 469; 66.2%; Pred. No. 1e-99; tive 62; Mismatches 89; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MODIFIED ANTIBODIES AND METHODS OF USE FILE REFERENCE: 037003-0280743
CURRENT APPLICATION NUMBER: PCT/US02/02373
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: 60/254,318
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                       APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Methods For Nucleic Acid Delivery
FILE REFERENCE: 2537,000012
CURRENT APPLICATION NUMBER: US/10/429,660
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 12
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Sequence 12, Application PC/TUS0202373
GENERAL INFORMATION:
                                                                                                                                                      Sequence 10, Application US/10429660
                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 317; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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NUMBER OF SEQ ID NOS: 17

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360 PSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTE 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGD 120
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65.1%; Pred. No. 3.3e-98;
tive 60; Mismatches 95; Indels 12; Gaps
                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Humanized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Complete heavy chain of Humanized 1D10 Ab US-09-618-380A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gingrich, Röger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
                                                                                                                              OTHER INFORMATION: C5E10 Heavy Chain Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 011823-004920US
CURRENT APPLICATION NUMBER: US/09/618,380A
CURRENT FILING DATE: 2000-07-18
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                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  Matches 312; Conservative
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                              Best Local Similarity
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19; Gaps

61.1%; Pred. No. 8.1e-89; tive 66; Mismatches 100; Indels

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123 YDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT 182
                                                                                                                                        64 LEWLGVIWSGGD-TDYNAAFISRLS|ISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIY 122
                                                                4 LGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKG 63
                                                                                     Best Local Similarity 61.1%
Matches 291; Conservative
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                                                                                                                                                80 AAFISRLSISKDNSKSQLFFKMNSLRAIDTAIYYCARNRGDIYYDFTYAMDYWGQGTSVT 139
                                                                                                                                                                   140 VSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALL 199
                                                                                                                                                                                                                                           228 -CPAPELLGGPSVFLFPPRFRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 Q-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH 258
                                                                                                                                                                                                                                                                                                                    174 QSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKT-HTCPP---- 227
                                                                                                                                                                                                                                                                                                                                                                       259 KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                               319 QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        379 VYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGDTDYN 79
                                                                                           15; Gaps
61.3%; Score 1565.5; DB 5; Length 446; 64.1%; Pred. No. 3.2e-93; Live 63; Mismatches 87; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 21085.002993
CURRENT APPLICATION NUMBER: PCT/US02/34420A
CURRENT FILING DATE: 2002-10-25
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PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
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PRIOR APPLICATION NUMBER: 60/391,478
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Ichikawa, Kimihisa
Kimberly, Robert P.
Koopman, William J.
Oshumi, Jun
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Buchsbaum, Donald J.
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SOFTWARE: PatentIn version 3.0
                   Best Local Similarity 64.1%
Matches 295; Conservative
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 Query Match
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APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: LOBUGIIO, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF FILE REFERENCE: 21085.0029P2
CURRENT APPLICATION NUMBER: PCT/USO2/35333A
120 -DSMITTDYWGQGTTLTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT 178
                                                                                              183 WNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS 242
                                                                                                                                                                                                                                                                                                                                                              303 DVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSP 362
                                                                                                                                                                                                                                                                                                                                                                                                179 WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVP- 237
                                                                                                                                                                                                                                 243 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLIPKVTCVVVDVSEDDP 302
                                                                                                                                                                                                                                                                   238 -----RDC-GCKPC-ICIVPEVS-}-SVFIFPPRPKPKDVLITLIPRVTCVVVDISKDDP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 IERTISKIKGLVRAPQVYILPPPAE¢LSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 IEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENY-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  423 KDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.7%; Score 1497.5; DB 1; Length 462; Best Local Similarity 61.1%; Pred. No. 8.1e-89; Matches 291; Conservative 66; Mismatches 100; Indels 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
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PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 102
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OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct

ORGANISM: Artificial Sequence

CT-US02-34420A-23

Query Match

us-09-770-916-2.rapn

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123 YDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT 182
                                    120 -DSMITTDYWGQGTTLIVSSAKTTPPSVYPLAPGSAAQINSMYLGCLVKGYFPEPVTVT 178
                                                                                                     183 WNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS 242
                                                                                                                                                                                                   243 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLIPKVICVVVDVSEDDP 302
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                                                                                                                           Matches 291; Conservative
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APPLICANT: Kimberly, Robert P.
APPLICANT: Kimberly, Robert P.
APPLICANT: Kopman, William J.
APPLICANT: LOBUGIIO, Albert S.
APPLICANT: Buchsbaum, Donald J.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APOPPOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF FILE REFERENCE: 21085.0029U7
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                                                                                                   64 LEWVATISSGGSYTYYPDSVKGRFTISRDNAKNTLYLQMSSLRSEDTAMYYCAR-RG--- 119
                                                                                                                                                                    123 YDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT 182
                                                                                                                                                                                                                  120 -DSMITTDYWGQGTTLIVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVT 178
                                                                                                                                                                                                                                                                183 WNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS 242
                                                                                                                                                                                                                                                                                        179 WNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVP- 237
                                                                        64 LEWIGVIWSGGD-TDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIY 122
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58.7%; Score 1497.5; DB 6; Length 462;
61.1%; Pred. No. 8.1e-89;
tive 66; Mismatches 100; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       423 KDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/286,132A CURRENT FILING DATE: 2003-01-22 PRIOR APPLICATION NUMBER: US 60/346,402
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PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
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SULT 7

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APPLICANT: Oshumi, Jun
APPLICANT: LoBuglio, Albert S.
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T
TITLE OF INVENTION: AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKG 63
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                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 21085.002906
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR PAPLICATION NUMBER: 60/391,478
PRIOR PELLING DATE: 2002-06-24
PRIOR PELLING DATE: 2001-11-01
PRIOR PELLING DATE: 2001-11-01
PRIOR PELLING DATE: 2001-11-01
PRIOR PELLING DATE: 2001-11-01
PRIOR PELLING DATE: 2001-13-04
PRIOR FILING DATE: 2001-05-02
PRIOR PELLING DATE: 2001-05-02
PRIOR PELLING DATE: 2001-05-02
                                                      APPLICANT: The UAB Research Foundation
; Sequence 23, Application US/10281479A
                                                                                                         Ichikawa, Kimihisa
Kimberly, Robert P.
Koopman, William J.
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SOFTWARE: PatentIn version 3.0
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Db 238RDC-GCKPC-ICTVPEVSSVFIFPPKENDVLTITLIPKVTCVVDISKDDP 286 Qy 303 DVQISWFVNNVEVHTAQTQTHREDXRSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSP 362 :	RESULT 10 US-10-384-933-9 ; Sequence 9, Application US/10384933 ; GENERAL INFORMATION; ; APPLICANT: SCRIZAWA, Nobufusa ; APPLICANT: Haruyama, Hideyuki ; APPLICANT: Tamaki, Ikuko ; APPLICANT: Tamaki, Ikuko ; APPLICANT: Tamaki, Ikuko ; APPLICANT: Tamaki, Tohnus, Applicant of Taxahashi, Tohnus	FILE REFERENCE: 980126CIP/HG CURRENT APPLICATION NUMBER: US/10/384,933 CURRENT APPLICATION NUMBER: US/205 FRIOR APPLICATION NUMBER: US/09/499,662 FRIOR APPLICATION NUMBER: ERRIFER APPLICATION NUMBER: US 09/053,583 FRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01 NUMBER OF SEQ ID NOS: 165 LENGTH: 464 TYPE: PRT CORGANISM: Mus musculus US-10-384-933-9	Query Match 57.7%; Score 1472; DB 6; Length 464; Best Local Similarity 59.1%; Pred. No. 3.6e-87; Matches 280; Conservative 73; Mismatches 105; Indels 16; Gaps 6; Qy 6 LLFCLYTFPSCYLSQYQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65	DD 6 IILFLVATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLE 65 QY 66 WLGVI-WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124	OY 125 FTXAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVÄGYFPESVTVTWN 184 123 NNWYFDVWGTGTTVTVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWN 182 QY 185 SGSLSSSVHTFPALLOSGLYTMSSSYFVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGP 244	Db 183 SGSLSSGVHTFPAVLQSDLYTLSSSVWPSSTWPSQTVTCNVAHPASSTKVDKKIVP 239 Qy 245 ISTINPCPPCKECHKCPAPNLEGGPSFFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV 304
ESVT	PRE IPP	RESULT 9 15-10-275-180A-23 Sequence 23, Application US/10275180A Sequence 23, Application US/10275180A Sequence 23, Application US/10275180A Sequence 23, Application US/10275180A Septicant: The UAB Research Foundation APPLICANT: The UAB Research Foundation APPLICANT: Ichikwa, Kimihisa APPLICANT: Kimberly, Robert P. APPLICANT: Koopman, William J. TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF FILE REFERENCE: 21085.0029US CURRENT APPLICATION NUMBER: US/10.275,180A	CURRENT FILING DATE: 2002-10-31 NUMBER OF SEQ ID NOS: 102 SOFTWARE: Patentin version 3.0 SEQ ID NO 23 LENGTH: 464 TYPE: PRT	Artificial DRMATION: DORMATION: S'	Query Match 58.7%; Score 1497.5; DB 6; Length 464; Best Local Similarity 61.1%; Pred. No. 8.1e-89; Matches 291; Conservative 66; Mismatches 100; Indels 19; Gaps 8; 4 LGLLECLVTFPSCVLSQVQLOSPSCSLSITCTVSGFSLTSYGVHWVRQSPGKG 63	b 5 LSLIF-LVLVKGVQCEVMLVESGGLVKPGGSLKLSCAASGFFFSSYVMSWVRQTPERR 63 'Y 64 LEWLGVIWSGGD-TDYNAAFISRLSISKDNSKSQLFFKNNSLRATDTAIYYCARNRGDIY 122 'III

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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLVRGYFPESVTVTWN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PASSTTVDKKLEPSGP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 QISWEVNNVEVHTAQTQTHREDYNSTİRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 QFSWFVDDVEVHTAQTQPREGENSTFRSVSELPIMHQNWLNGKEFKCRVNSAAFPAPIE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVTCVVVDVSEDDPDV 304
                                                                                                                                                                                                                                                                                                                                                              SYGVHWVRQSPGKGLE 65
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:: :|::| ||||
HHTEKSLSHSPGK 462
                                                                                                                                                                                                                                                                                                                                        dels 16; Gaps
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                                                                                                                                                                                                                 JS 09/053, 583
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243 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPRVTCVVVDVSEDDP 302

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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                           SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Ponath, Paul
APPLICANT: Bruce Keyt
TITLE OF INVENTION: IMMONOGLOBULIN DNA CASSETTE MOLECULES,
TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS OF
TITLE OF INVENTION: USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 LTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 PSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSED 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 PRVPI-TQNPCPPLKECPPCAAPDLLGGPSVFIFPPRIKDVLMISLSPMVTCVVVDVSED 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 DPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 SPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEE 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IYYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 ------VIVSSAKTIAPSVYPLAPVGGTIGSSVTLGCLVKGYFPEPVT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAVLGLLFCLVTLPNCVLSRL-----21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40; Indels 117; Gaps
411 TQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.3%; Score 1462.5; DB 6; Length 361; 59.8%; Pred. No. 1.1e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: immunoglobulin cassette protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 286; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: MPIO1-244P2RM
CURRENT APPLICATION NUMBER: US/10/272,899A
CURRENT FILING DATE: 2002-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/350,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/392,364 PRIOR FILING DATE: 2002-06-26
                                                                                                                                  Sequence 82, Application US/10272899A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Leader-Mu_WT_60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                APPLICANT: O'Keefe, Theresa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                         GENERAL INFORMATION:
                                                                                                      :-10-272-899A-82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3-10-272-899A-82
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LENGTH: 361
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Sequence 14, Application PC/TUS0236107

CT-US02-36107-14

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241 PSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSED 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 ------RKC--CVECPPCPAPPV-AGPSVFLFPPRPKDTLMISRTPBVTCVVVDVSHE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 DPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEE 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 SWNSGALTSGVHTFPAVLQSSGLYSLSSVYTVPSSNFGTQTYTCNVDHKPSNTKVDKTVE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 IWSGGDTDYNAAFI-SRLSISKDNSKSQLFFKMNSLRATDTAIYYCAR-----NRGDI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 YYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LVALLRGVQCQVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 NYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Score 1457; DB 1; Length 474; 58.6%; Pred. No. 3.4e-86; tive 72; Mismatches 104; Indels 25
                                                                                                   CURRENT APPLICATION NUMBER: PCT/US02/36107 CURRENT FILING DATE: 2002-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/10/292,088
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                                                 TITLE OF INVENTION: ANTIBODIES TO CD40 FILE REFERENCE: ABX-PF/3 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/348,980
                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/348,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/10292088; GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: ORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003-03-14
                                                                                                                     2002-11-08
APPLICANT: ABGENIX, INC. APPLICANT: PFIZER PRODUCTS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                 PRIOR FILING DATE: 2001-11-09
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SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2003-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280; Conservative
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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DNSKSQLFFKMNSLRATDTAIYYCARNRGD 120

VQPSQSLSITCTVSGFSLTSYGVHWVROSP 60

42; Indels 117; Gaps

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; TYPE: PRT ; ONCANISM: Homo sapiens	Matches 284; Conservative 35; Mismatch
Çat ∸	QY 1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVV
<pre>vative 72; Mismatch SQVQLXOSGPGLVOPSOSLSIT</pre>	QY 61 GKGLEWLGVIWSGGDTDYNAAFISRLSISKD
GVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAV	1
Qy 70 IWSGGDTDYNAAFI-SRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDI 121 :	22
OY 122 YYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTV 181	65
	125
	184
301 DPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHODWMSGKEFKCKVNNKDLP	OY SOLESTISKLKGLVRAQVILLPPPABQLSR : : :
35	Qy 421 NYKDTAPVLDSDGSYFIYSKLNMKT\$KWEKTI : :: : 304 NYKNTATVLDSDGSYFMYSKLRVQK\$TWERG
421	RESULT 15 PCT-US02-36107-70 ; Sequence 70, Application PC/TUS0236107 ; GENERAL INFORMATION:
RESULT 14 1S-10-272-8994-80 1S-10-28-80-80 1S-10-28-80 ; APPLICANT: ABGENIX, INC. ; APPLICANT: PFIZER PRODUCTS INC. ; TITLE OF INVENTION: ANTIBODIES TO CD40 ; FILE REFERENCE: ABX-PF/3 PCT ; CURRENT APPLICATION NUMBER: PCT/USO2/36107 ; CURRENT PELIANG DATE: 2002-11-08 ; PRIOR PILING DATE: 2001-11-09 ; NUMBER OF SEQ ID NOS: 147 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 70 ; LENGTH: 466 ; TYPE: PRT ; ORCANISM: HOMO Sapiens PCT-USO2-36107-70	
CURRENT FILING DATE: 2002-10-17 PRIOR APPLICATION NUMBER: 60/350, 166 PRIOR PILING DATE: 2001-10-19 PRIOR APPLICATION NUMBER: 60/303 364	Query Match 56.9%; Score 1451; Best Local Similarity 58.5%; Pred. No. 8. Matches 280; Conservative 72; Mismatche
PRIOR FILING DATE: 2002-06-26 NUMBER OF SEQ ID NOS: 110 SOFTWARE: FastSEQ for Windows Version 4.0	QY 1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQ
LENGTH: 361 TYPE: PRT ORGANISM: Artificial Sequence	Qy 61 GKGLEWLGVIWSGGDTDYNAAFISRUSISKDN
OTHER INFORMATION: immunoglobulin cassette protein sequence OTHER INFORMATION: Leader-Mu_FCRII_61 JS-10-272-899A-80	Qy 121 IYYDFTYAMDYWGQGTSVTVSSAKTTPPSVYP : 1:

YPLAPGCGDTTGSSVTLGCLVKGYFPESVT 180 VFIFPPNIKDVLMISLTPKVTCVVVDVSED 300 IRVVSTLPIQHQDWMSGKEFKCKVNNKDLP 360 TVPSSTWPSQTVTCSVAHPASSTTVDKKLE 240 || | |:|||||:||
TVTSNTWPSQTITCNVAHPASSTKVDKKIE 124 :|: |||||:: || | :|:||||| ||: KKEFSLTCMITGFLPAEIAVDWTSNGRTEQ 303 RKDVSLTCLVVGFNPGDISVEWTSNGHTEE 420 ONSKSQLFFKMNSLRATDTAIYYCARNRGD 120 | ||:| ||:| |:||: | |||:|||| ||:| |DTSKNQFSLKLNSVTAADTAVYYCAR-KGG 119 121 IYYDFTYAMDYWGQGTSVTVSSAKTTPPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVT 180 181 VTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWDSQTVTCSVAHPASSTTVDKKL 239 VQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60 TDSFSCNVRHEGLKNYYLKKTISRSPGK 478 |:|:| ||||| |: GSLFACSVVHEGLHNHLTTKTISRSLGK 361 nes 113; Indels 14; Gaps ; DB 1; Length 466; 8.2e-86; gg ŏ δy

56.9%; Score 1452.5; DB 6; Length 361; 59.4%; Pred. No. 5e-86;

Query Match Best Local Similarity

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179 VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTKVDKTV 238
                                                                              360 PSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTE 419
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3.4 D.D.DIEKMISKWKCODBEDOVYHIDDSPERMIKNOVSTHOLVKGEYDSDIAVEWESNGODE 407		420 ENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 4/8	408 NNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466
: :	WINGT FURT TOUT	ENYKDTAPVLDS	NNYKTTPPMLDS
9.70	5	420	408

parch completed: June 18, 2003, 16:48:36 bt ime : 59.3933 secs

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Sequence 4, Appli
Sequence 6, Appli
Sequence 127944,
Sequence 54066, A
Sequence 126419,
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                                                                                                                                                         June 18, 2003, 16:44:27; Search time 296.065 Seconds (without alignments) 1040.930 Million cell updates/sec
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/cgn2_6/Ptodata/1/paa/JS085_COMB.pep:*
11. /cgn2_6/Ptodata/1/paa/JS085_COMB.pep:*
12. /cgn2_6/Ptodata/1/paa/JS081_COMB.pep:*
13. /cgn2_6/Ptodata/1/paa/JS089_COMB.pep:*
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16. /cgn2_6/Ptodata/1/paa/JS091_COMB.pep:*
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12. /cgn2_6/Ptodata/1/paa/JS095_COMB.pep:*
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14. /cgn2_6/Ptodata/1/paa/JS098_COMB.pep:*
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/cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-653-755A-4
US-09-653-755A-6
US-09-791-537-127944
US-09-791-537-54066
US-09-791-537-126419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4569144 seqs, 644733110 residues
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                                                                                                    OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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daximum DB seq length: 2000000000
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chance to have a	re greater than or equal to the score of the result being printed,	stribution.
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Sequence 26476, A Sequence 40387, A Sequence 26475, A Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1231, A Sequence 12560, Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 15, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9, Appli 9,	Length 478;
91-537-26476 91-537-26476 91-537-26475 91-537-60389 91-537-620389 91-537-620389 91-537-620389 91-537-620389 91-537-620389 91-537-12231 91-537-12231 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-28655 91-537-89130 91-537-89130 91-537-89130 91-537-89130 91-537-89130	2552; DB 21;
US-09-7-7-9-7-9-7-9-7-9-7-9-7-9-7-9-7-9-7-	Score
336 21 405 21 405 21 405 21 336 21 336 21 468 3 468 7 468 12 468 12 468 12 468 12 469 8 12 440 21 440 100.08;	
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1802 1798 1798 1799 1799 1799 1799 1799 1799	SEQ ID NO 2 LENGTH: 476 TYPE: PRT ORGANISM: n -09-770-916-2
RESULT THIFTELY APPELL THIFTELY APPELL THIFTELY APPELL THIFTELY APPELL THIFTELY APPELL	; SEQ ID ; LENG; ; ORGAL US-09-77(

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; Sequence 6, Application US/09653755A; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 VTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPA 197
                                                                                                                                                                                                                                                                                241 PSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTFKVTCVVVDVSED 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 YNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTS 137
                                                                                                                                                                                        181 VTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                        241 PSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSED 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 DPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLP 360
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                                                                                                                                                            61 GKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGD 120
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                                                                   1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60
                                                                                                                  1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSP 60
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                       0; Gaps
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81.6%; Score 2083.5; DB 20; Length 454;
Best Local Similarity 84.8%; Pred. No. 1.8e-161;
Matches 391; Conservative 26; Mismatches 35; Indels 9;
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APPLICANT: LaMarche, Arthur
APPLICANT: Jelinek, Thomas
TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for
TITLE OF INVENTION: Phosphotyrosine-Containing Proteins
FILE REFERENCE: 724650-3
                    0; Indels
100.0%; Pred. No. 7.8e-200; tive 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 12
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                         Matches 478; Conservative
      Best Local Similarity
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78 YNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTS 137
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                                                                                            258 HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 317
                                                                                                                                                                                                                                                                                                                                                             378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
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                     114 LTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPA 173
                                                                      198 LLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC 257
                                                                                                                                                                                                                  234 HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Gaps
OTHER INFORMATION: Description of Artificial Sequence:Amino acid OTHER INFORMATION: sequence for heavy chain of recombinant antibody OTHER INFORMATION: with C-terminal histidine tag sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LaMarche, Arthur APPLICANT: Jelinek, Thomas TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for TITLE OF INVENTION: Phosphotyrosine-Containing Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
NUMBER OF SEQ ID NOS: 153055
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 SQALLQSGLYTMSSSYTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPC 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 VLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.0%; Score 2067; DB 21; Length 474; 83.8%; Pred. No. 4.3e-160; Live 29; Mismatches 38; Indels 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        435 YFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 126419, Application US/09791537 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 389; Conservative
                                                      APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-791-537-126419
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 54066
LENGTH: 474
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APPLICANT: Denzer, Joseph
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
KURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                         1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 1010 | 10
318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
                                                                                                                                      378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
                                                                                                                                                                              79 NAAFISRLSISKDNSKSQLFFKMNSLRAIDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 198
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81.6%; Score 2082; DB 21; Length 457;
Best Local Similarity 84.3%; Pred. No. 2.4e-161;
Matches 388; Conservative 31; Mismatches 37; Indels 4;
                                                                                                                                                                                                                                                                                438 YSKLNMKTSKWEXTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                     Sequence 127944, Application US/09791537 GENERAL INFORMATION:
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IS-09-791-537-127944
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LENGTH: 457
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ORGANISM: Mus musculus

SEQ ID NO 126419 LENGTH: 475

439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478

Sequence 54066, Application US/09791537

8-09-791-537-54066

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TYPE: PRT

US-09-791-537-126419

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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                             241 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 300
323 HREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYIL 382
                     383 PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLN 442
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                                                                                                                                                                                 443 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                    301 MKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 336
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                                                                                                                                                                                                                                                                                                                               Sequence 40387, Application US/09791537 GENERAL INFORMATION:
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TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 PALLOSGLYTMSSSYTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCPPCK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                              256 ECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 BCHKCPAPNLEGGPSVFIFFPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSY 435
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                                                                                                                                                                                                                                                                                              196 PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCK 255
                                                                                                                                                                                         76 TDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQG 135
                                                                                                                                                                                                                                                                          136 TSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF 195
                                                                                                    17 VLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSG-GD 75
                                                                                                                                           17 VQSQVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRTGQGLEWIGEIYPGSGN 76
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                                                             5; Gaps
          79.3%; Score 2024.5; DB 21; Length 475; 82.3%; Pred. No. 1.3e-156; tive 30; Mismatches 47; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 336;
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100.0%; Pred. No. 1.4e-138;
tive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                                                                 Matches 381; Conservative
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                     Query Match
Best Local Similarity
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LENGTH: 336
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Tue Jul 1 18:40:54 2003

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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
                                                                      121 NLEGGPSVFIFPPNIKDVLMISLIPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQIQH 180
                                                                                                                                              324 REDYNSTIRVVSTLPIQHQDWMSGK#FKCKVNNKDLPSPIERTISKIKGLVRAPQVYILP 383
                                                                                                                         384 PPAEQLSRKDVSLICLVVGFNPGDI$VEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNM 443
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEO ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                Sequence 62004, Application US/09791537 GENERAL INFORMATION:
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APPLICANT: Bionomix, Inc.
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                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bionomix, Inc.
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US-09-791-537-62004
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LENGTH: 336
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                              143 AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
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                                                                                                                                                                                      70.3%; Score 1793; DB 21; Length 404; 100.0%; Pred. No. 9.8e-138; tive 0; Mismatches 0; Indels 0.
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CURRENT APPLICATION NUMBER: US/09/791,537
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CURRENT APPLICATION NUMBER: US/09/791,537
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                 CURRENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 153055 SOFTWARE: Patentin version 3.0
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NUMBER OF SEQ ID NOS: 153055
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                                                                                                                           ORGANISM: Mus musculus
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S-09-791-537-40389
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                                                                         SEQ 1D NO 26475
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61 LYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 120
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                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                           69.7%; Score 1778; DB 21; Length 336; 98.8%; Pred. No. 1.3e-136;
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                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                       0; Mismatches
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             CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: CARP-0009
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19910917
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SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
                                                                                     SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                          Matches 332; Conservative
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FILE REFERENCE: 261/210
                                                                                                                                                                               ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                            SEQ ID NO 40377
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121 DHYCLDYWGGGTTLTVSSAKTTAPSVYPLAPVGGDTTGSSVTLGCLVKGYFPEPVTLTWN 180
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                                                                                                                                                                      75; Indels 12;
                                                                                                                                  Length 468;
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One Liberty Place - 46th Floor
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PatentIn Release #1.0, Version #1.25
                                                                                                                                68.6%; Score 1751; DB 3; 69.0%; Pred. No. 3.3e-134;
                                                                                                                                                                        60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/743,329
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/303,569
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                  I: 468 amino acids
AMINO AÇID
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                                                                                                                                                      Best_Local Similarity 69.0 Matches 327; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                          ; MOLECULE TYPE: protein US-07-743-329-7
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us-09-770-916-2.rapm

US/08/485,686

APPLICATION NUMBER:

FILING DATE: 07 CLASSIFICATION:

07-JUN-1995

US 07/743,329

NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712

FILING DATE: 17-SEP-1991 ATTORNEY/AGENT INFORMATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 7 SEQUENCE CHARACTERISTICS: LENGTH: 468 amino acids

TELEFAX:

amino acid linear

TOPOLOGY:

REFERENCE/DOCKET NUMBER:

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66 WLGVI-WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
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NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: CARP-0009
TELEPROMUNICATION INPORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3100
TELEPHONE: SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                               LENGTH: 468 amino acids
                                                                                                                                                                                                                                                                                                                          327; Conservative
                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-303-569-7
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66 WLGVI-WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
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                                                         68.6%; Score 1751; DB 8; Length 468; 69.0%; Pred. No. 3.3e-134; tive 60; Mismatches 75; Indels 1:
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                                                                                          Matches 327; Conservative
, MOLECULE TYPE: protein US-08-485-686-7
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Best Local Similarity
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Job time : 299.065 secs

Woodcock Washburn Kurtz Mackiewicz & Norris

One Liberty Place - 46th Floor

Philadelphia

USA

COUNTRY:

PA

STATE:

CORRESPONDENCE ADDRESS:

ADDRESSEE:

STREET:

NUMBER OF SEQUENCES:

APPLICANT: Athwal, Diljeet S. APPLICANT: Emtage, John S. TITLE OF INVENTION: Humanised Antibodies

Sequence 7, Application US/08485686 GENERAL INFORMATION:

13-08-485-686-7

ESULT 15

APPLICANT: Adair, John R.

PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

PC-DOS/MS-DOS

OPERATING SYSTEM:

SOFTWARE:

COMPUTER:

IBM PC compatible

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

us-09-770-916-2.rapb

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(without alignments)
1149.899 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

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RESULT 1 US-09-795-515-7 Sequence 7, Application US/09795515 Publication No. US20030039645A1 GENERAL INFORMATION: APPLICANT: Addair, John R. APPLICANT: Emtage, John S. TITLE OF INVENTION: Humanised Antibodies CORRESPONDENCE ADDRESS: APPLICANT: Emtage, John S. TITLE OF INVENTION: Humanised Antibodies CORRESPONDENCE ADDRESS: APPLICANT: Emtage, John S. TITLE OF INVENTION: Humanised Antibodies CORRESPONDENCE ADDRESS: APPLICANT: Philadelphia STREET: One Liberty Place - 46th Floor CITY: Philadelphia STATE: PA COUNTRY: USA COMPUTER: Elbepy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-OOS SOFTWARE: Patentin Release #1.0, Versi COMPUTER: IBM PC compatible OPERATION PRICATION NUMBER: US/09/795,515 FILING DATE: O1-MAY-1997 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 35,719 REFERENCE/DOCKET NUMBER: 35,719 REFERENCE/DOCKET NUMBER: 35,719 REFERENCE/OMOUNICATION INFORMATION: TELEPHONE: TELEPHONE: C15, 568-3439 INFORMATION POR SEQ ID NO: 7: SEQUENCE CHARACTERIFICS: LENDTH: 468 amino acids	mino acid : linear YPE: prote

-09-795-515-7

Query Match

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185 SGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGP 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCK 255
                                                                                                                                                                                                                                                                                                                                                         316 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 WLGVI-WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
                         136 TSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF 195
                                                                                                               256 ECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEV 315
                                                                                                                                                                                                                                                                                            294 HTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSY 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 FTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWN 184
76 TDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQG 135
                                                                                                                                                                                                     6 ILLFLVATATGVHSQVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.7%; Score 1472; DB 9; Length 464; 59.1%; Pred. No. 7.6e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Serizawa, No. US20030103976Alufusa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 9, Application US/10216484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haruyama, Hideyuki
Nakahara, Kaori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Publication No. US20030103976A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-216-484-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-216-484-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
                                                                                                                                                                                                                                                                                                                              66 WIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCAR----YYD 120
                                                                                                                                                                                                                                                                                                                                                                                              185 SGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 ISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 QISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 RTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKD 424
                                                                                                                                                                                                                                                                                                     125 FTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWN 184
                                                                                                                                                                                                               66 WLGVI-WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 VLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWS-GGD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94; Indels 24; Gaps
                                                                             76; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (0)...(0)
OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415 TEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 TAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.7%; Score 1472; DB 9; Length 456; 60.0%; Pred. No. 7.5e-75;
                             68.3%; Score 1742; DB 9; Length 468; 68.8%; Pred. No. 7.1e-90; Live 60; Mismatches 76; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/903,327A CURRENT FILING DATE: 2001-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: 09/613,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09903327A Patent No. US20020164333A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Nemerow, Glen R.
                                                           Best_Local Similarity 68.83
Matches 326; Conservative
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.09-903-327A-2

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5-09-903-327A-2

Query Match

LENGTH: 456

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SEQ ID NO 2

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79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Gaps
                                                                                                   APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 57.1%; Score 1456.5; DB 9; Length 452; Best Local Similarity 60.1%; Pred. No. 5.4e-74; Matches 277; Conservative 68; Mismatches 105; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P1085R4-1A
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US-09-726-258-71; Sequence 71, Application US/09726258; Publication No. US20030021790A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/234,182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WinPatin (Genentech)
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258 HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 317

318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377 438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478

378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437

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                                                                                                                                                                                                                                                                                                         256 ECHKCPAPNLEGGPSVFIFPPNIKDVLMISLIPKVTCVVVDVSEDDPDVQISWFVNNVEV 315
                                                                                                                                                                                                                                                                                                                                                                                                     130 LGOPN----TLICFVDNIFPPVINITWLRNSK------SVTDGVYETSFL----VN 171
                                                                                          90 KDNSKSQLFFKMNSLR--ATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV----- 138
                                                                                                                                                                                         139 ---TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR 375
                                                                                                                                             172 RDHS----FHKLSYLTFIPSDDDIYDC------KVEHWGLEEPVLKHWEPEIP 214
30 LVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGDTDYNAAFISRLSIS 89
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71; Indels 55; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:PCB223 OTHER INFORMATION: recombinant MHC class II heterodimer
                                                                                                                                                                                                                                                              TITLE OF INVENTION: Immune Medators and Related Methods FILE REFERENCE: 014058-005670US
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,837
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/191,274
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: US 60/204,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILLING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 60/264,003
PRIOR FILLING DATE: 2001-01-23
SOFFMARE: PATENTING VET: 1.29
SOFFMARE: PATENTING VET: 2.1
                                            Sequence 93, Application US/09815837 Patent No. US20020082411A1
                                                                                                                                                         APPLICANT: Zhu, Shirley
APPLICANT: Arimilli, Subhashini
                                                                                                                                                                                                                 APPLICANT: Wang, Aijun
APPLICANT: Corixa Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 62.4% Matches 289; Conservative
                                                                                                                                APPLICANT: Carter, Darrick
                                                                                                       GENERAL INFORMATION:
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                         -09-815-837-93
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SULT 6
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMBAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 PGKGLEWLGVIW-SGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAVIGILFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLT-SYGVHWVRQS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSY 435
                                                                                                   449 APQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSY 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.6%; Score 1445; DB 9; Length 476; Best Local Similarity 57.8%; Pred. No. 2.5e-73; Anders 281; Conservative 72; Mismatches 115; Indels 18; Gaps
                                                                                                                                                 436 FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMUNOSUPPRESANTS"
12
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                                                                                                                                                                                                                                                                                               Sequence 12, Application US/10124905
Patent No. US20020166136A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Anderson, Darrell R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: /vs c. 7021
TELEPHONE: /vs c. 7021
TELEPHONE: /vs c. 7031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-10-124-905-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                  US-10-124-905-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Henderikx, Maria P.G.
TITLE OF INVENTION: MOCIN-1 Specific Binding Members and Methods of Use Thereof
FILE REFERENCE: DYX-015.1 US/09/822, 698A
CURRENT APPLICATION NUMBER: 0S/09/822, 698A
                                                                                                                                                                               61 PGKGLEWIGSFYSSSGNTYYNPSLK$QVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
                                                                                                                                                                                                                              119 ----GDIYYDFTYAMDYWGQGTSV‡VSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKG 173
                                                                                                                                                                                                                                                                                                                              60 PGKGLEWLGVIW-SGGDTDYNAAFI$RLSISKDNSKSQLFFKMNSLRATDTAIYYCARNR 118
                                                                                                                                                                                                                                                         174 YFPESVTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASS 232
                                                                                                                                                                                                                                                                                                                                                                                     233 TTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTC 292
                                                                                                                                                                                                                                                                                                                                                                                                               293 VVVDVSEDDPDVQISWEVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKC 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 KVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEW 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        413 TSNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTI 472
                                                                          1 MAVLGLLFCLVTFPSCVLSQVQLKQ$GPGLVQPSQSLSITCTVSGFSLT-SYGVHWVRQS 59
                                                                                                20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWL-GVIWSGGDTDY 78
56.6%; Score 1445; DB 9; Length 476;
57.8%; Pred. No. 2.5e-73;
Live 72; Mismatches 115; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1 US-09-822-698A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.4%; Score 1440; DB 10; Length 451; 59.9%; Pred. No. 4.5e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/538,913 PRIOR FILING DATE: 2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 26, Application US/09822698A ; Patent No. US20020146750A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: artificial sequence
                                     Matches 281; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 59.9%
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 112
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 SRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 SLSPGK 476
                   Best Local Similarity
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 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNR---GD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 IYYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                        139 TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 198
                                                                                                                                                                                                               258 HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 317
                                                                                                                                                                                                                                                                                                                        233 --CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
                                                                                                                                                                                                                                                                                                                                                                      318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 410
                                         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGGVWD---PIDYWGQGTLV 117
                                                                                                               199 LQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYG--VHWVRQSPGKG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 ILLFLVAVATRVLSQVQLQESGPALVKPTQTLTLTCTFSGFSLSTRGMSVNWIRQPPGKA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 56.4%; Score 1439.5; DB 10; Length 475; Best Local Similarity 58.7%; Pred. No. 5e-73; Matches 281; Conservative 72; Mismatches 111; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                       438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: U5/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/488,376
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Patent No. US20020001798al
GENERAL INFORMATION:
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257 CHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVH 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 VTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 VIVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 ---CPAPELLGGPSVFLFPFRRDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVEVH 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 TAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRA 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 LLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKE 256
                                                                                                                                            360 PSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTE 419
240 EPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSE 299
                             14 EPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKRKDTLMISRTPEVTCVVVDVSH 296
                                                                                                              300 DDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDL 359
                                                                                                                                                                                                                                                                                           357 PAPIEKTISKAKGOPREPQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AEVQLVESGGGLVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGNTI 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 SQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVI-WSGGDTD 77
                                                                                                                                                                                                                                                                                                                                                  420 ENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

56.2%; Score 1434; DB 9; Length 470;

Best Local Similarity 59.3%; Pred. No. 1e-72;

Matches 274; Conservative 67; Mismatches 105; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/020,786 CURRENT FILING DATE: 2002-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: anti-TF heavy chain US-10-020-786-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10020786 Publication No. US20030073164A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klimowski, Laura
Reilly, Dorothea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Simmons, Laura C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 11
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TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES

APPLICANT: PFIZER PRODUCTS INC

GENERAL INFORMATION:

FILE REFERENCE: PC23019A

Sequence 9, Application US/10153382 Publication No. US20030086930A1

S-10-153-382-9

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TITLE OF INVENTION: and Treatment 70 IW-SGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCAR-NRGDIYYDFTY 127 188 LSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPIS 246 353 ISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 412 9 128 AMDYWGQGTSVTVSSAKTTPPSVYPIJAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGS 187 126 -- DYWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA 183 307 SWFVNNVEVHTAQTQTHREDYNSTIRİVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERT 366 367 ISKIKGLVRAPQVYILPPPAEQLSRKÞVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTA 426 10 LVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGV Gaps 427 PVLDSDGSYFIYSKLNMKTSKWEKTD\$FSCNVRHEGLKNYYLKKTISRSPGK 478 20; 15; 56.1%; Score 1430.5; DB 9; Length 450; 58.9%; Pred. No. 1.5e-72; Live 72; Mismatches 103; Indels 15; Length 464; 56.1%; Score 1432; DB 9; Length 4 58.5%; Pred. No. 1.3e-72; tive 69; Mismatches 107; Indels TITLE OF INVENTION: and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259 Sequence 220, Application US/09996288 Patent No. US20020177126A1 CURRENT FILING DATE: 2002-05-22 PRIOR APPLICATION NUMBER: 60/293042 PRIOR FILING DATE: 2001-05-23 SOFTWARE: PatentIn version 3.1 Matches 276; Conservative *NUMBER OF SEQ ID NOS: 39 SOFTWARE: PatentIn Ver. 2.1 Best_Local Similarity 58.9% Matches 272; Conservative Scott, Koenig ORGANISM: Homo sapiens APPLICANT: Young, James APPLICANT: Scott, Koeni ; ORGANISM: Homo sapiens US-09-996-288-220 Best Local Similarity GENERAL INFORMATION: US-09-996-288-220 LENGTH: 464 US-10-153-382-9 SEQ ID NO 220 TYPE: PRT SEQ ID NO 9 Query Match TYPE: PRT Query Match

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APPLICANT: Scott, Roenig
APPLICANT: Scott, Moenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Adminstering/Dosing Anti-RSV Antibodies for Prophylaxi
TITLE OF INVENTION: and Treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 ---CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 288
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                                                                                                                                    198 LLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKE 256
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                                                                                                       78 YNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTS 137
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20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYG--VHWVRQSPGKGLEWLGVIWSGGDTD 77
                                                    1 QVTLRESGPALVKPTQTLTLTCTFSGFSLSTAGMSVGWIRQPPGKALEWLADIWWDGKKD 60
                                                                                                                                                                                                                                        56.1%; Score 1430.5; DB 9; Length 450; 58.9%; Pred. No. 1.5e-72; tive 72; Mismatches 103; Indels 15;
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FILE REFERENCE: 10271-048-999
CURRENT APPLICATION NUMBER: US/09/996,265
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 220, Application US/09996265 Publication No. US20030091584Al GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 272; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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LENGTH: 450
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Search completed: June 18, 2003, 16:58:01 Job time : 46.9803 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - protein search, using sw model Run on:

June 18, 2003, 16:42:37 ; Search time 23.4972 Seconds (Without alignments) 598.546 Million cell updates/sec

Title:

2552 1 MAVLGLLFCLVTFPSCVLSQ......RHEGLKNYYLKKTISRSPGK 478 US-09-770-916-2 Perfect score:

Scoring table: BLOSUM62 Sequence:

262574 seqs, 29422922 residues Gapop 10.0 , Gapext 0.5 Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Semental Conductor		` r	, , , ,	, ,	, α	Sequence 18, Appl	. ~			71,	71,	- 1	12	10,0	+ α	<u>،</u> د		2	-	16.	18,	25	14	1	Segmence 18. Appl	2, 4
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JS-09-054-255-2 JS-09-296-005-14 JS-09-296-005-16	US-09-296-005-18 US-08-487-550-4 US-08-523-894-8 PCT-US96-13152-4	US-08-704-744-81 US-09-049-672A-8 US-09-301-593-30 US-09-301-593-18	US-07-934-373C-23 US-08-437-642B-23 US-08-146-206C-23 US-08-466-151-8	US-08-466-163B-8 US-08-157-101A-7 PCT-US93-07832-23
-60-SU	US-09- US-08- US-08- PCT-US	US-08- US-09- US-09- US-09-	US-07- US-08- US-08- US-08-	US-08- US-08- PCT-US
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ALIGNMENTS

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nant iewic	l; DB 2; 3.6e-132; ches 75;
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Application Use Application Use Application Use Formation In T: Joiliffe, I: Zivin, Rober T: Zivin, Rober T: Athwal, Dil INVENTION: CIF SEQUENCES: Woodcock: One Liberty Philadelphia P. A. One Liberty Philadelphia P. One Liberty Philadelphia P. One Liberty Philadelphia READABLE FORM: READABLE FORM: RESPECTION OF SYSTEM: POPPLICATION DATE: DATE: NATION NUMBER: PATENTION NUMBER: PATENTION NUMBER: CICATION NUMBER:	۸a
GENERAL INFORMATION: APPLICANT: Jolliffe, Linds APPLICANT: Jolliffe, Linds APPLICANT: Jolliffe, Linds APPLICANT: Addit, John R. APPLICANT: Addit, John R. APPLICANT: Addit, John R. APPLICANT: Athwal, Dilject TITLE OF INVENTION: CD3 § NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS: ADDRESSE: WOGGOCK Wask STREET: ONCE Liberty Plact CITY: Philadelphia STATE: PA COUNTRY: PA COUNTRY: PA COUNTRY: PA COUNTRY: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EMP PC COMPATION OF SOFTHARE: PATCHING SYSTEM: DC-DCS SOFTHARE: PATCHING SYSTEM: US/OF SOFTHARE: PATCHING SYSTEM: US/OF SOFTHARE: DO-OCT-1991 ATTORNEY/AGENT INFORMATION: AS PRILICATION NUMBER: US/OF FLING DATE: 10-OCT-1991 ATTORNEY/AGENT INFORMATION: PATCHELEPONNUICATION INFORMATION: TELEFONNUICATION INFORMATION: TYPE: MINO ACID TOPOLOGY: linear MOLECULE TYPE: protein NB-116-247-7	Simi 7;
RESULT 1 US-08-116-247-7 Sequence 7, 9 Patent No. 59 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: CORRESPOND APPLICANT: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R MEDIUM TY: COMPUTER R COMPUTER R MEDIUM TY: COMPUTER R	Query Match Best Local Matches 32
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                                                                                                                             125 FTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWN 184
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                                                       66 WLGVI-WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
6 IFLLLLSVTAGVHSQVQLQQSGAELARPGASVKASCKASGYTFTRYTMHWVKQRPGGGLE 65
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One Liberty Place - 46th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Humanised Antibodies NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/303,569B
FILING DATE: 07-SEP-1994
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08303569B Patent No. 5859205
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Athwal, Diljeet S. APPLICANT: Emtage, John S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19103
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121 DHYCLDYWGGGTTLTVSSAKTTAPSVYPLAPVGGDTTGSSVTLGCLVKGTFPEFVTLTWN 180
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                                                                                 6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425 TAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 TEPVLDSDGSYEMYSKLEVEKKNWVERNSYSCSVVHEGLHNHTTKSFSRTPGK 468
68.3%; Score 1742; DB 2; Length 468;
68.8%; Pred. No. 1.9e-131;
Live 60; Mismatches 76; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Townsend and Townsend and Crew
                                             60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             011823-004901
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FILING DATE: 01-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/859,583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30,223
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith, William M.
                                               Matches 326; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                           Best Local Similarity
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TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
 415-326-2400
                                                        446 amino acids
                                                                                    single
                                                                                                              MOLECULE TYPE: peptide
                                                                    amino acid
                                                                                                 linear
                                                                               STRANDEDNESS:
TELEPHONE:
                                                                                                 TOPOLOGY:
                                                        ENGTH:
                                                                                                                            US-08-397-411-7
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80 AAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSVT 139 140 VSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALL 199 200 Q-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH 258 259 KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318 319 QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378 228 -CPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 286 379 VYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY 438 347 VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 406 20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGCDTDYN 79 85; Indels 15; Gaps 61.9%; Score 1580.5; DB 3; Length 446; 64.6%; Pred. No. 1.5e-118; Live 63; Mismatches 85; Indels 15; 439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478 Best Local Similarity 64.6% Matches 297; Conservative Query Match a à à á á

18-08-353-400-36 ESULT

SOFTWARE: Patentin Release #1.0, Version #1.25 (EFO) CURRENT APPLICATION DATA: OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 36, Application US/08353400 Patent No. 5665357 GENERAL INFORMATION: IBM PC compatible TITLE OF INVENTION: PROTEINS COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NUMBER OF SEQUENCES: COMPUTER: APPLICANT:

APPLICATION NUMBER: US/08/353,400 GB 9324819.3 UMBER: GB 9411089.7 03-JUN-1994 FILING DATE: 03-JUN-1994 INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS: FILING DATE: 03-DEC-1993 PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: (APPLICATION NUMBER: CLASSIFICATION: FILING DATE:

66 WLG-VIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124 125 FTYAMDYWGQGTSVTVSSAKTTPPS\\ YPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWN 184 185 SGSLSSSVHTFFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGP 244 240 ----RDC-GCKPC-ICIVPEVS---SVEIFPPRFRDVLITLIFFFKVTCVVDISKDDPEV 290 245 ISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV 304 305 QISWFVNNVEVHTAQTQTHREDYNST|IRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIE 364 365 RTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENVKD 424 6 LLFCLVTFPSCVLSQVQLKQSGPGL\QPSQSLSITCTVSGFSLTSYG\UWVRQSPGKGLE 65 Gaps 425 TAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478 Indels 16; Length 464; 59.4%; Score 1515; DB 1; 60.3%; Pred. No. 2.7e-113; tive 72; Mişmatches 100; 464 amino acids Matches 286; Conservative single MOLECULE TYPE: protein TYPE: STRANDEDNESS: SIL Similarity ; MOLECULE TYF US-08-353-400-36 LENGIH: Query Match est Local δy qq δλ g δ g δλ ద δλ g δ g ŏ 셤 ŏ

SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO) CURRENT APPLICATION DATA: US/08/353,40 GB 9324819.3 GB 9411089.7 OPERATING SYSTEM: PC-DOS/MS-DOS ; Sequence 33, Application US/08353400 ; Patent No. 5665357 E: Floppy disk IBM PC compatible TITLE OF INVENTION: PROTEINS INFORMATION FOR SEQ ID NO: 33: FILING DATE: 03-DEC-1993 PRIOR APPLICATION DATA: 03-JUN-1994 SEQUENCE CHARACTERISTICS: LENGTH: 445 amino acids COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of PRIOR APPLICATION DATA: APPLICATION NUMBER: (STRANDEDNESS: single CLASSIFICATION: 424 APPLICATION NUMBER: APPLICATION NUMBER: NUMBER OF SEQUENCES: amino acid GENERAL INFORMATION: FILING DATE: FILING DATE: COMPUTER: US-08-353-400-33 APPLICANT:

linear

TOPOLOGY:

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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                            79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                                                                                                               199 LQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH 258
                                                                                                                                                                                                                                                                                                                                                                                                                                         259 KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318
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                                                                                                                                                                                                                                                                                     139 IVSSAKITPPSVYPLAPGCGDITGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHIFPAL 198
                                                                                                                                 20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLG-VIWSGGDTDY 78
                                                                                                                                                        16; Gaps
                                                     Query Match 59.0%; Score 1506; DB 1; Length 445; Best Local Similarity 61.3%; Pred. No. 1.3e-112; Matches 282; Conservative 69; Mismatches 93; Indels 16
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APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
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FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
RECISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
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FILING DATE: 16-MAY-1995
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5686600
GENERAL INFORMATION:
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   MOLECULE TYPE: protein
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                         -08-353-400-33
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266. GISVIVSSAKITIPPSVYPLAPGSRSAAQINSMVILGCLVKGYFPEPVIVTWNSGSLSSGV 325
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                                                                                                                                                                                                                                                                                                                                                                                                                               193 HTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        253 PCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLIPKVTCVVVDVSEDDPDVQISWFVNN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                494 RPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTN 553
                                                                                                                                                                                                                                                                                                                                                                                                     76 -TDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 GTSVTVSSAKTTPPSVYPLAPGCGDT--TGSSVTLGCLVKGYFPESVTVTWNSGSLSSSV 192
                                                                                                                                                                                                                                                                                                              18 LSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGD-- 75
                                                                                                                                                                                                                                                                   90; Indels 24; Gaps
                                                                                                                                                                                                                   Query Match 58.2%; Score 1484; DB 1; Length 599; Best Local Similarity 60.5%; Pred. No. 1.1e-110; Matches 282; Conservative 70; Mismatches 90; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433 GSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
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APPLICANT: Carozzi, Michael G.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
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STREET: 7 Skyline Drive
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Patent No. 6069301
GENERAL INFORMATION:
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                    TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO: 18:
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919-541-8615
                                                                                         599 amino acids
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                                                                SEQUENCE CHARACTERISTICS:
                  919-541-8689
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                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                              amino acid
                                                                                                                                     linear
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TELEPHONE:
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                                                                                                                                TOPOLOGY:
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                                                                                                                                                                                US-08-442-542-18
                                                                                         LENGTH:
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3174 Porter Drive
                                                                                                                      IBM Compatible
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                                                                                                                                                                                                                                                                                                                 NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 473 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 57.7%
Best Local Similarity 58.8%
Matches 285; Conservative
                                                                                                                                          DOS
                                                                                                                                                                                                            HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650-845-4166
                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PANCTUT01
                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                 Palo Alto
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LIBRARY: PAIN.
NO. 1513264
                                                                                                                                                                                                                            CLASSIFICATION:
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                                                     USA
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                                                                                                                                                                                                                                                                               FILING DATE:
                                                                      94304
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                                                                                                                        COMPUTER:
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                                                   COUNTRY:
STREET:
                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 VEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWNSGKEFKCKVNNKDLPSPIERTISKIKG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 HTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 PCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNN 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 LVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSD 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 LSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGD-- 75
                                                                                                                                                                                                                                                                                                                   tch 58.2%; Score 1484; DB 3; Length 599;
al Similarity 60.5%; Pred. No. 1.1e-110;
282; Conservative 70; Mismatches 90; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS NUMBER OF SEQUENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 GSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
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                                                                                                              CGC 1750
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillman, Jennifer L.
Lal, Preeti
Tang, Y. Tom
                                                                      NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC
                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
                                                                                                                                                            TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
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                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               LENGTH: 599 amino acids IYPE: amino acid
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-765-469-18
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                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                    linear
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                                        FILING DATE:
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Query Match

Matches

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59 SPGKGLEWLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARN- 117 61 PPCKGLEWIGYIYYSGSTLYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARDD 120 118 ----RGDIYYDFTYAMDYWGQGTSVTV|SSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGY 174 175 FPESVTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASST 233 236 KVDKRVEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPTLMISRTPEVTCV 288 294 VVDVSEDDPDVQISWFVNNVEVHTAQFQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCK 353 354 VNNKDLPSPIERTISKIKGLVRAPQV†ILPPPABQLSRKDVSLTCLVVGFNPGDISVEWT 413 234 TVDKKLEPSGPISTINPCPPCKECHKCPANLEGGPSVFIFPPNIKDVLMISLTPKVTCV 293 414 SNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTIS 473 1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVH--WVRQ 58 57.7%; Score | 1471.5; DB 4; Length 473; 58.8%; Pred. No. 8.2e-110; tive 70; Mismatches 111; Indels 19; Gaps SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: US/09/049,672A PF-0497 39,132 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555

474 RSPGK 478

ADDRESSEE:

IS-09-049-672A-4

APPLICANT: APPLICANT: APPLICANT:

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California
NUMBER OF SEQUENCES:
                                                        1 DNA Way
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                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                    SOFTWARE:
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                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 LQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVP------RDC-GCKPC- 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            259 KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 PDSVKGRFTISRDNAKNTLXLQMSGLKSEDTAMYYCARRITTVVLTDYYAMDYWGQGTSV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 TVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 VYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWDGQPAENYKNTQRIMNTDGSYFVY 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIWSGGD-TDY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.2%; Score 1460; DB 6; Length 447; 60.7%; Pred. No. 6.3e-109; tive 69; Mismatches 98; Indels 14
                                                                                                                       APPLICANT: LADNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL TITLE OF INVENTION: LWMUNOTHERAPHY USING SINGLE CHAIN OLYPEPTIDE BINDING MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408 SKLDVQKSNWEAGDTFTCSVLHEGLHDHHTEKSLSHSPGK 447
                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/40,440
FILING DATE: 1-APR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 71, Application US/09027449
Patent No. 6025158
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 512,910
FILING DATE: 25-AR-1990
APPLICATION NUMBER: 299,617
FILING DATE: 19-JAN-1989
APPLICATION NUMBER: 92,110
APPLICATION NUMBER: 92,110
APPLICATION NUMBER: 902,971
APPLICATION NUMBER: 902,971
FILING DATE: 01-SEP-1986
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                                                                                                                                                                                                 NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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            469 LSPGK 473
                                                                                                               atent No. 5455030
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378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 HKCPAPULEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1111 | 111111:111 | 11111 | 1:11111111 | 1:1:1: 1:1: 1111 | 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1:1: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVOLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%; Score 1456.5; DB 3; Length 452; 60.1%; Pred. No. 1.2e-108;
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                         Genentech, Inc.
                                                                                                                                                                                                                                                          South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650/225-5530
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Amino Acid
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                                                                                                                     CORRESPONDENCE ADDRESS:
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us-09-770-916-2.rai

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79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
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                                       438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                         PE: 3.5 inch, 1.44 Mb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  Genentech, Inc., Hsei, Vanessa
Koumenis, Iphigenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-Jul-1998
CLASSIFICATION: 514
                                                                                                                                                                     Sequence 71, Application US/09121952A Patent No. 6458355
                                                                                                                                                                                                                                                                   APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TITLE OF INVENTION: WITH ANTI-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genentech, Inc. STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: DNA way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Love, Richard B.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94080
                                                                                                                                                   US-09-121-952A-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 LQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Mismatches 105; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.1%; Score 1456.5; DB 4; Length 452; 60.1%; Pred. No. 1.2e-108;
                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P1085R3-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20-Feb-1998
CLASSFFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PC-DOS/MS-DOS
                                                            Sequence 71, Application US/09026985
Patent No. 6133426
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
                                                                                                                       APPLICANT: Gonzalez, Tania R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                           Genentech, Inc.
                                                                                                                                                                                                                                                                                                 South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 60.13
Matches 277; Conservative
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                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                         ADDRESSEE: Genc. 1 DNA Way
                                                                                                                                                                                                                                                                                                                  California
                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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S-09-026-985-71
                                                                                                    GENERAL INFORMATION:
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                                           JS-09-026-985-71
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                                                                                                                                                                                                                                                                                                                    STATE:
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                       RESULT 11
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352 QVYTLPPSREEMTKNQVSLTCLVKG#YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411 5, METHODS OF TREATING INFLAMMATORY DISEASES WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES 11; Gaps 57.1%; Score 1456.5; DB 4; Length 452; 60.1%; Pred. No. 1.2e-108; tive 68; Mismatches 105; Indels 11; ထ

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                           179 LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEFKSCDKT-HTCPP---- 233
                                                                                                                                                                                     352 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL 411
199 LO-SGLYIMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC 257
                                                                                 258 HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 317
                                                                                                                       234 --CPAPELLGGPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 291
                                                                                                                                                                  318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
                                                                                                                                                                                                                                                   378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
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APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
                                                                                                        438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                          E: 3.5 inch, 1.44 Mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
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APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/074330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1085R4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 71, Application US/09234340A
Patent No. 6468532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Love, Richard B. REGISTRATION NUMBER: 34,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
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INFORMATION FOR SEQ ID NO: 71:
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STATE: California
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Amino Acid
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                   79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                                                                           318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
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                                                                                                                                                                                                                                                                                                                                          199 LQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC 257
                                                                                  20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVI-WSGGDTDY 78
                                                                                                           57.1%; Score 1456.5; DB 4; Length 452;
60.1%; Pred. No. 1.2e-108;
tive 68; Mismatches 105; Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/487,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/08487550 Patent No. 6113898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                   Matches 277; Conservative
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                              Similarity
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            Query Match
                                    Best Local
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us-09-770-916-2.rai

; MOLECULE TYPE: protein US-08-487-550-12

TOPOLOGY:

Gaps h 56.6%; Score 1445; DB 3; Length 476; Similarity 57.8%; Pred. No. 1.1e-107; Sl, Conservative 72; Mismatches 115; Indels 1 Matches 281; Conservative Query Match Best Local

1 MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLT-SYGVHWVRQS 59

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PGKGLEWLGVIW-SGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNR 118

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----GDIYYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKG 173 174 YFPESVTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASS 232

TTVDKKLEPSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTC 292

293 VVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKC 352

353 KVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEW 412

413 TSNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTI 472

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473 SRSPGK 478

471 SLSPGK 476

Sequence 12, Application US/08523894 Patent No. 6136310 GENERAL INFORMATION: IS-08-523-894-12

APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy

CORRESPONDENCE ADDRESS NUMBER OF SEQUENCES:

BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street Alexandria ADDRESSEE:

COMPUTER READABLE FORM: 22314-3187 USA COUNTRY:

SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

Floppy disk

MEDIUM TYPE:

JMBER: US/08/523,894 06-SEP-1995 APPLICATION NUMBER: FILING DATE:

012712-165 NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 01.2 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620 INFORMATION FOR SEQ ID NO: 12: ATTORNEY/AGENT INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 467 amino acids JECCUMAN. 703-02.
TELEPHONE: 703-02. MOLECULE TYPE: protein amino acid linear CLASSIFICATION: TOPOLOGY: US-08-523-894-12

60 PGKGLEWLGVIW-SGGDTDYNAAFI\$RLSISKDNSKSQLFFKMNSLRATDTAIYYCARNR 118 61 PCKGLEWIGYIYGSGGGTNYNPSLNNRVSISIDTSKNLFSLKLRSVTAADTAVYYCASN- 119 119 GDIYYDFTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPES 178 | 120 ---ILKYLHWILXWGQGVLVTVSSAŞTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP 176 238 KLEPS-GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVD 296 179 VIVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDK 237 297 VSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNN 356 357 KDLPSPIERTISKIKGLVRAPQVYIL PPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNG 416 1 MAVLGLLFCLVTFPSCVLSQVQLKQ\$GPGLVQPSQSLSITCTVSGFSLT-SYGVHWVRQS 56.0%; Score 1429.5; DB 4; Length 467; 57.9%; Pred. No. 1.8e-106; Live 74; Mismatches 110; Indels 19; Gaps Best Local Similarity 57.98 Matches 279; Conservative

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Search completed: June 18, 2003, 16:49:18 Job time: 25.4972 secs

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Chimeric 4H6 anti-
Humanised 1D10 ant
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                                                                                                                                      June 18, 2003, 16:41:53 ; Search time 65.7921 Seconds (without alignments) 968.107 Million cell updates/sec
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                                                                                                                                                                                                                                                                                    1 MAVLGLLFCLVTFPSCVLSQ......RHEGLKNYXLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDSZ/gcgdata/geneseg/genesegp-embl/AA1989.DAT:*/SIDSZ/gcgdata/geneseg/genesegp-embl/AA1990.DAT:*/SIDSZ/gcgdata/geneseg/genesegp-embl/AA1991.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                            908470 seqs, 133250620 residues
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                                                                                          OM protein - protein search, using sw model
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Listing first 45 summaries
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AAR47450
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ABB76126
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AAW05829
AAB81972
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Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                     BLOSUM62
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                                                                                                                                                                                                                                                                                                                                       Scoring table:
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                                                                                                                                           Run on:
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AAR76085 AAR76085 AAR76085 AAV2801 AAR66758 AAV3801 AAR80937 AAR80937 AAR80937 AAR80937 AAR80937 AAR80937 AAR80939 AAR809897 AAR809897 AAR809897 AAR809897 AAR809897 AAR809897 AAR809897 AAR809897 AAR809897 AAR899643 AAR896408 AAR896408 AAR896408 AAR896409 AAR896408 A	ALIGNMENTS 1. 454 AA. heavy chain. ody; 4G10; phosphotyrosine; cancer; coded by CAR" 6. 6. 5. OGY INC.	
11 1515 59.4 464 13 1497.5 58.9 445 14 1493.5 58.7 464 18 1480.5 58.0 448 18 1480.5 58.0 448 18 1479.5 58.0 448 18 1472 57.7 464 22 1472 57.7 464 22 1472 57.7 464 23 1472 57.7 464 24 1471.5 57.7 464 25 1470.5 57.7 464 26 1459.5 57.1 452 37 1456.5 57.1 452 38 1456.5 57.1 452 38 1456.5 57.1 452 39 1456.5 57.1 452 31 1456.5 57.1 452 31 1456.5 57.1 452 32 1445.5 57.1 452 33 1445.5 56.8 466 34 1445.5 56.8 466 35 1445.5 56.8 475 37 1445.5 56.8 475 38 1439.5 56.4 475 48 1439.5 56.4 475 48 1434.5 56.4 475 49 1439.5 56.4 475 49 1433.5 56.2 475	RESULT 1 ABB76124 ID ABB76124 ID ABB76124; XX AC ABB76124; XX DT 15-JUL-2002 (first,entry) XX DE Recombinant 4G10 antibody heavy ch XX Monoclonal antibody; antibody; 4G1 XX OS Unidentified. XX OS Unidentified. XX OS Unidentified. XX OS UNIDENTIFIED. XX PT Misc-difference 5 FT Misc-difference 5 FT Misc-difference 5 FT Misc-difference 5 FT MO200218443-A2. XX PD 07-MAR-2002. XX PD 07-MAR-2002. XX PD 01-SEP-2000; 2000US-0653755. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX PD NOSTPATE BIOTECHNOLOGY INC. XX	WPI; 2002-393728/42. N-PSDB; ABL56966.

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378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 VTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 EVQLQQSGPELVKPGASVMISCRTSAYTFTENTVHWVKQSHGESLEWIGGINPYYGGSI- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVI--WSGGDTD 77
Novel recombinant monoclonal antibody with 4010-hybridoma type specificity useful in diagnostic procedures, especially for detection of phosphotyrosine-containing proteins in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              including cancers, to identify cellular substrates for tyrosine kinases, for affinity purification of phosphotyrosine-containing proteins and for determining the tyrosine phosphorylation status of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in diagnosis of a variety of diseases
                                                                                                                                                                                                                     The present sequence is the protein sequence for the heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.6%; Score 2083.5; DB 23; Length 454; 84.8%; Pred. No. 1.1e-127; tive 26; Mismatches 35; Indels 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       one or multiple proteins in a given cell or tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
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                                                                                                                                                      Claim 6; Page 55-56; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biological/medical research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002 (first entry)
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Matches 391; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258
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198 LLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 YNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 VTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 LLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specificity useful in diagnostic procedures, especially for detection of phosphotyrosine-containing proteins in a sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the protein sequence for the heavy chain of a recombinant monoclonal antibody having 4G10 hybridoma-type specificity. The heavy chain has been amended by the addition of a histidine tag at the C-terminal end. CDNA encoding the amended heavy chain was obtained by PCR amplification of 4G10 hybridoma CDNA and by site-directed mutagenesis. This heavy chain CDNA was cloned into a eukaryotic vector and, with a vector for the 4G10 Hight chain, was used to produce a secreted, functional recombinant monoclonal antibody in transfected mammalian cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biological/medical research, in diagnosis of a variety of diseases including cancers, to identify callular substrates for tyrosine kinases, for affinity purification of phosphotyrosine-containing proceins and for determining the tyrosine phosphorylation status of one or multiple proteins in a given cell or tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombinant antibody is useful for detecting the presence of phosphotyrosine-containing proteins in a sample, for use in biological/medical research, in diagnosis of a variety of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.6%; Score 2083.5; DB 23; Length 462; 84.8%; Pred. No. 1.1e-127; tive 26; Mismatches 35; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel recombinant monoclonal antibody with 4G10-hybridoma type
                                                                                                                                                                                                                                                                                                                                Jelinek T;
                                                                                                     /note= "encoded by CAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 57-59; 60pp; English.
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                Lamarche A,
                                                                                                                                                                                                                                                                                            (UPST-) UPSTATE BIOTECHNOLOGY INC.
                                                                                                                                                                                                                      30-AUG-2001; 2001WO-US26926
                                                                                                                                                                                                                                                      01-SEP-2000; 2000US-0653755
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                                                                                        Misc-difference 5
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                Unidentified.
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                                   Synthetic.
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318 AQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377

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Gaps

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DB 9; Length 341; 0; Indels

Score 1789.5; DB 9 Pred. No. 1.1e-108; 0; Mismatches

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143 AKTIPPSVYPLAPGCGDITGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSG 202
                                                                                                                                                                                          203 LYIMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECHKCPA 262
                                                                                                                                                                                                          263 PNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV----QISWFVNNVEVHT 317
                                                                                                                                                                                                                                                                     318 AQTQTHREDYNSTIRVVSTLPIQHQÞWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAP 377
                                                                                                                                                                                                                                                                                                                                                                          378 QVYILPPPAEQLSRKDVSLTCLVVGRNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
                                                                                                                                                                                                                                                                                                                                                                                           residue 297 of the heavy chain has been changed to Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                       438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                       70.1%;
98.5%;
                                                                                                 Matches 336; Conservative
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                                                                                    Local Similarity
                                           341 AA;
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                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
378 QVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFI 437
                                                             Immunoglobulin; class gamma; antibody; immune response; Fc receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified antibodies (Abs) having an altered Fc region with altered binding affinity for an Fc receptor esp. Fc-gamma-R1 may have the following residues replaced: 234, 235, 236 and 237; 235 by Glu, and at least one of the others by Ala. Those with altered binding affinity for Clq may have an altered CH2 domain in which one of the following residues of the heavy chain have been changed to a residue with a different side chain; 318 (changed to Val) 320 and 322 (changed to Gln). Those with altered lytic properties, as compared with unmodified Ab may have an altered CH2 domain where
                                                                                                                                                                                                                                                                                                                                                effector molecule; constant region; heavy chain; complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "This residue is Leu in mutant EL235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified IgG class antibody - having at least one aminoacid residue in the constant portion altered to alter an effector
                                                                                                                      438 YSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                        Sequence encoded by mouse 1gG gamma 2b gene.
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                             AAP83200 standard; Protein; 341 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burton DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         98..119
/label= hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example; Fig 3; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87GB-0006425.
87GB-0018897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88WO-GB00211.
                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87GB-0028042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88WO-GB00211
88GB-0025480
                                                                                                                                                                                                                                                                        06-MAR-1992 (first_entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235..341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winter GP, Duncan AR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1988-285543/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAN82456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1988;
01-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO8807089-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1988
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New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in a vivo therapy and diagnosis
OK3T; light chain; humanised antibddies; CDR-grafting.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= signal peptide
                                                                                                                                                                                                                                                                                Monoclonal antibody OK3T heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= light chain
                                                                                                                                      AAR13061 standard; Protein; 468 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2b; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emtage JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90WO-GB02017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90WO-GB02017.
                                                                                                                                                                                                                               03-OCT-1991 (first entry)
```

function

#XXXXXX##X

¥ X 8 X 4 X 4 X 4 X 4 X 4 X

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The OK3T heavy chain sequence was deduced from the CDNA sequence isolated from a library prepared from OK3T producing cells. The library was screened with a probe complementary to a region in the mouse IgG2a constant domain region. The OK3T sequence was used in CDR-grafting experiments to prepare humanised antibodies.
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4;
                                                                                                                                                                                                                                                                                                                                                           121 DHYCLDYWGGGTTLTVSSAKTTAPSVYPLAPVGGDTTGSSVTLGCLVKGYFPBFVTLFWN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                    185 SGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGP 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 ISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 RTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 WIGYINPSRGYTNYNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAVYYCAR----YYD 120
                                                                                                                                                                                                                                                                                                                                  125 FTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 --TIKPCPPC----KCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDV 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 QISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIE 364
                                                                                                                                                                                                                                     66 WLGVI-WSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
                                                                                                                                     6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65
                                                                                                                                                                                     6 IFLLLLSVTAGVHSQVQLQQSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRPGQGLE 65
                                                                                        12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 TAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.6%; Score 1751; DB 12; Length 468; 69.0%; Pred. No. 4.9e-106; Live 60; Mismatches 75; Indels 12.
                                                                    Best Local Similarity 69.0%
Matches 327; Conservative
468 AA;
  Sequence
                                                  Query Match
```

A fragment of the heavy chain (VH + CH1) from the anti-snake small neurotoxin monoclonal antibody M(alpha)2-3 was PGR-amplified from hybridoma-derived CDNA using primers AAQ48039 and AAQ48040. A light chain fragment (VL + CL) was amplified from the same source using primers AAQ48041 and AQ48042. The two amplified fragments were inserted into the same vector; the H-chain fragment was inserted (in-frame) between codons of 7 of the phoA coding sequence and the L-chain fragment was inserted into a cassette which contained a phoA s-D sequence, a signal peptide and the first 6 codons of phoA. The cassette was positioned between the termination codon and

New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or

Example 1; Fig 3A; 37pp; French.

therapeutic use

Boulain J, Ducancel F, Gillet D, Menez A; (COMS) COMMISSARIAT ENERGIE ATOMIQUE

(BOUL/) BOULAIN J.

1-FEB-1992; 09-FEB-1993; 18-AUG-1993. EP556111-A.

WPI; 1993-260351/33

N-PSDB; AAQ48037

93EP-0400323 92FR-0001505 construct is expected to to encode a hybrid protein comprising two identical Ab-derived units. The invention also covers hybrid proteins containing two different Ab-derived units (i.e. to produce bispecific antibodies). When a toxic protein is used in place of phoA, the hybrid molecules can be used as cell-targetting

therapeutic agents.

469 AA;

transcription termination sequence of phoA. The fusion

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79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                          139 TVSSAKTIPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 198
                                                                                                                                                                                                    199 LQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH 258
                                                                                                                                                                                                                                                                 259 KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318
                                                                                                                                                                                                                                                                                                                             319 QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378
                                                                                                                                                                                                                                                                                                                                                                                       379 VYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY 438
                                                             20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGVIW-SGGDTDY 78
                                                                              11; Gaps
67.7%; Score 1727.5; DB 14; Length 469; 69.6%; Pred. No. 1.7e-104;
tive 60; Mismatches 69; Indels 11;
                                     320; Conservative
                       Best Local Similarity
            Query Match
                                                                                                                                                                                                                          q
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                                                                        δλ
                                                                                                                                   δλ
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anti-snake small neurotoxin antibody; heavy chain; IgG2; immunoglobulin; bispecific bivalent antibody; cell-targetting;

cytotoxic agent.

Peptide

Region Region Region Region Region

/label= signal_peptide Location/Qualifiers

/label= variable

. 236

constant

'label-

- constant

/label

.362 ..252

joining

/label= constant

.469

Monoclonal antibody M(alpha)2-3 Heavy-chain.

08-FEB-1994 (first entry)

AAR40384;

AAR40384 standard; Protein; 469 AA

SSULT 5 AR40384 4

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q δ οy pp δλ qq δ g δλ 370 VYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMY 429 67 LGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFT 126 132 GGFGYWGGGTLATVSAAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSG 191 127 YAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSG 186 7 LFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEW 66 | || || :|:|:||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| Indels 10; Gaps Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region; transform; myeloma cell; light chain; tumour. The sequences (AAO54651-52) show the light and heavy chain cDNAs of murine T84.12. The T84.12 antibody is directed against the tumour marker carcinoma embryonic antigen, and is useful for antigen - has murine variable and human constant regions, also DNA encoding it and transformed myeloma cells New chimaeric T84.12 antibody active against carcinoembryonic tumour imaging and immunotherapy.

The amino acid sequence given in the specification has been incorrectly identified as a nucleic acid sequence, therefore unacceptable characters have been represented as an 'N'.

The amino acid sequence given below has been derived from the cDNA, by the indexer. DB 15; Length 477; 439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478 Wu A, Yang YHJ; 67.0%; Score 1711; DB 15; 69.1%; Pred. No. 2e-103; tive 53; Mismatches 83; Fischer R, Paxton R, Shively JE, AAR47450 standard; Protein; 477 AA Claim 1; Page 17; 27pp; English. 93WO-US05709. 92US-0904074. (first entry) Matches 326; Conservative (CITY) CITY OF HOPE. 1994-007204/01. 184.12 Heavy chain. Best Local Similarity 477 AA; N-PSDB; AAQ54652 (YANG/) YANG Y 24 - JUN - 1994 15-JUN-1993; 15-JUN-1992; W09325237-A 23-DEC-1993 Synthetic. AAR47450; Sequence Query Match AAR4745(RESULT

SLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPIS 246 307 SWEVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERT 366 367 ISKIKGLVRAPQVYILPPPAEQLSRÅDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTA 426 9 77 DYNAAFISRLSISKDNSKSQLFFKMN\$LRATDT-AIYYCARNRGDIYYDFTYAMDYWGQG 135 20 QVQLKQSGPGLVQPSQSLSITCTVSGRSLTSYGVHWVRQSPGKGLEWLGVIWSG---GDT 76 construct mouse/human chimeric antibodies. KSI/4 is a murine antibody which binds to surface antigens on adenocarcinoma cells and the use of human C regions avoids immunological problems during treatment. 247 TINPCPPCKECHKCPAPNLEGGPSV#IFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQI 20; Gaps 427 PVLDSDGSYFIYSKLNMKTSKWEKT \$\daggerupskepspck 478 65.4%; Score 1669; DB 10; Length 447; 68.5%; Pred. No. 1e-100; Live 52; Mismatches 74; Indels 20; monoclonal and The sequence encodes the heavy chain of MAb KS1/4, used to KS1/4; chimeric antibody; heavy cha|in variable region; Recombinant DNA cpds. producing antibodies - mon chimeric derived from monoclonal antibody KS1/4. Bumol TF, Gadski RA, Weigel BJ; Chimeric antibody heavy chain variable region. AAP93037 standard; protein; 447 AA Claim 6; page 50; 89pp; English. 89EP-0303814. 14-MAR-1990 (first entry) (ELIL) ELI LILLY AND CO. Matches 317; Conservative WPI; 1989-311203/43. Best Local Similarity 447 AA; N-PSDB; AAN91659 18-APR-1989; Beavers LS, 25-APR-1989 EP338767-A. 187 Sequence Query Match Mus. QY, g g pp

us-09-770-916-2.rag

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1997
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                256 ECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEV 315
                                                                                                                                 228 ---KCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEV 284
                                                                                                                                                                            316 HTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVR 375
                                                                                                                                                                                                                                      376 APQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSY 435
                                                        196 PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCK 255
                                                                       136 TSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel anti-death receptor 4 antibodies useful for treating cancer and immune related disorders such as rheumatoid arthritis, sjogren's syndrome, Grave's disease and diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention relates to an anti-Death receptor 4 (DR4) antibody. The antibodies of the invention are useful for inducing apoptosis in mammalian cancer cells such as colon cancer cells and for treating an immune-related disease in a mammal such as arthritis and autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-Death receptor 4; DR4; antibody; apoptosis; cancer; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.5%; Score 1596; DB 22; Length 476; Best Local Similarity 63.8%; Pred. No. 6.1e-96; Matches 305; Conservative 65; Mismatches 96; Indels 12;
                                                                                                                                                                                                                                                                                                 436 FIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                   Chimeric 4H6 anti-DR4 antibody heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dodge KH, Kim KJ;
                                                                                                                                                                                                                                                                                                                                                                                                          AAB49243 standard; protein; 476 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Fig 18; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi AJ, Chuntharapai A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0322875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2000; 2000WO-US14599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-041145/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200073349-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB49243;
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SCULT 8 **NB49243**

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361 SPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEE 420
                                                                                                                                                                                                                                       126 SLLSYHSMNFWGQGTSVTVSSAKTTGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTV 185
                                                                                                                                                                                                                                                                                      182 TWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE 240
                                                                                                                                                                                                                                                                                                                    241 PSGPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSED 300
                                                                                                                                                                                                                                                                                                                                                                                                                146 PKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLP 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 APIEKTISKAKGOPREPOVYTLPPSREEMTKNOVSLICLVKGFYPSDIAVEWESNGOPEN 418
                                                                                         66 WLGVIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDF 125
                                                                                                                          126 T----YAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTV 181
6 LLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLE 65
                      6 IILFLVATATGVHSXVQLKESGPGLVAPSQSLSITCTVSGFSLTSYGVHWVRQPPGKGLE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 NYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B-cell lymphoma; humanised antibody; bispecific antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myeloma; leukaemia; hybridoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Variable_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Humanised 1D10 antibody heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW05829 standard; Protein; 446 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98..105
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-US02754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340..446
/label= CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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AAB81972;

(IOWA-) IOWA IMMUNOTHERAPY INVESTIGATORS 01-MAR-1995; XX XX

5002 TC:04:07 T

1

Gingrich R, Link BK,

(PROT-) PROTEIN DESIGN LABS INC.

WPI; 1996-412742/41.

New bispecific antibody reactive with both T or NK cells and mailgnant B cells - also their humanised forms and hybridomas producing them, useful for treating or preventing leukaemia, Lymphoma and myeloma

Example 4; Fig 4e; 85pp; English.

XIXEXETETXXXXCCCCCCCCC

The humanised ID10 antibody heavy chain (AAW05829) includes a variable region (see also AAW05823) consisting of human R3.5HG heavy chain variable region framework and complementarity determining regions from the murine ID10 antibody specific for a 28/32 kba antigen found on the surface of malignant B-cells. It can be coexpressed with humanised ID10 light chain (see also AAW05828) in mammalian host cells. Bispecific antibodies can be constructed that include a first binding fragment comprising humanised M291 heavy and light chain variable regions (see also AAW05826, AAW05830), and a second binding fragment comprising humanised ID10 heavy and light chain variable regions (see also AAW05820, AAW05830), and a second variable regions. Such antibodies are reactive with both T or NK cells and malignant B cells, and have therapeutic and diagnostic

446 AA; Sequence

Gaps 15; DB 17; Length 446; 87; Indels 61.3%; Score 1565.5; DB 364.1%; Pred. No. 5.5e-94; 63; Mismatches Matches 295; Conservative Best Local Similarity Query Match

140 VSSAKTIPPSVYPLAPGCGDITGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALL 199 a δŽ ò ద δ

319 QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378 287 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ

379 VYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY 438

ŏ g δλ

> 439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478

JB8197

AAB81972 standard; Protein; 581 AA

The present invention describes an antibody, which can react specifically with gangiloside GD2, and is transplanted with a human type complementation-determining domain (CDR), or its fragments. The antibody and its derivatives are useful in diagnosis and therapy of tumours, particularly cancer diagnosis. The present sequence is a protein used in the exemplification of the invention. Human type complementation-determining domain transplanted antibody and derivatives against ganglioside GD2, useful in diagnosis and therapy of e.g. tumours, has low antigenicity, little side effects but potent Ganglioside; GD2; complementation determining region; CDR; antibody; Ganglioside GD2 specific antibody ‡elated protein SEQ ID NO: 31. Example 3; Page 111-114; 123pp; Japanese. Nakamura K, (KYOW) KYOWA HAKKO KOGYO KK 29-SEP-2000; 2000WO-JP06773. 03-JUL-2001 (first entry) Hanai N, Shitara K, WPI; 2001-266163/27. activity in cancer WO200123573-A1. mouse; cancer. 05-APR-2001

DB 22; Length 581; Indels 60.9%; Score 1554.5; DB 22. 63.9%; Pred. No. 3.8e-93; ative 64; Mismatches 89; Matches 294; Conservative Best Local Similarity Query Match

581 AA;

Seguence

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AAR76088;

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66 WLG-VIWSGGDTDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYD 124
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Sequence

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125 FTYAMDYWGQGTSVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWN 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94GB-0011089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAb 55.1 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Boot C,
Wright AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-215262/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZENE ) ZENECA LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09515382-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blakey DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rose MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR76085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 59.4%; Score 1515; DB 16; Length 464; Best Local Similarity 60.3%; Pred. No. 1.1e-90; Matches 286; Conservative 72; Mismatches 100; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAD 55.1 (ECACC 93081901) recognises the colorectal tumor-associated antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, ScFv or v-min humanized 55.1 constructs have been expressed in myeloma
                                                                                                                                                                                                                                           Antigen binding structure; complementarity determining region; CDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigen binding structures containing CDRs recognising the CA55.1
                                                                                                                                                                                                                                                        CASS.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAD; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paterson DS;
       439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478 ·
                           /label= Mat_protein
/note= "claim 3, page 97-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copley CG, Hall SM,
                                                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig.15; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                    AAR76088 standard; Protein; 464 AA
                                                                                                                                                                                                                                                                                                           humanized antibody; immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-GB02610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94GB-0011089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93GB-0024819.
                                                                                                                                                                                  21-NOV-1995 (first entry)
                                                                                                                                                                                                                MAb 55.1 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Boot C, Wright AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-215262/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells and E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ94037.
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29-NOV-1994; 03-JUN-1994; 03-DEC-1993;

Blakey DC,

Rose MS,

WO9515382-A 08-JUN-1995

Peptide Protein

Mus sp.

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351 KTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKN 410
                                                                                                                                                                183 SGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVP--- 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 QFSWEYDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 RTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKD 424
185 SGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGP 244
                                                                                                                                                                                                                                                                                      245 ISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDV 304
                                                                                                                                                                                                                                                                                                                                                                      240 ----RDC-GCKPC-ICTVPEVS---SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 QISWFVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An antigen binding structure is based on the CDRs (given in AAR76078-84) of the heavy (AAR76085) and light (AAR76086) chains of MAD 55.1 (ECACC 93081901), which recognises the colorectal tumor-associated antigen CA55.1. It is optionally humanized and in the form F(ab')2, F(ab)', Fab, Fv, scFv or V-min, and is produced in transgenic animals or plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            425 TAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 TQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA55.1; colorectal cancer; tumor-associated antigen; hybridoma, monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copley CG, Hall SM, Paterson DS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 97-98; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR76085 standard; Peptide; 445 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            humanized antibody; immunotoxin.
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N-PSDB; AAS97062

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79 NAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIYYDFTYAMDYWGQGTSV 138
                                                                                                                                                                                                                                                               TVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPAL 198
                                                                                                                                                                                                                                                                                                                                       LQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTINPCPPCKECH 258
                                                                                                                                                                                                           259 KCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTA 318
                                                                                                                                                                                                                                                                                    QTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQ 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 VYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIY 438
                                                                                                                                   TRAIL; TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation; autoimmune disease; systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia; Addison disease; scleroderma; Goodpasture's syndrome; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
                                                                                                            20 QVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLG-VIWSGGDTDY
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumour necrosis factor-related apoptosis-inducing ligand receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergy; arteriosclerosis; myocarditis; cardiomyopathy;
glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
                                                                                   16;
                                               Length 445;
                                                                                 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 SKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                      58.9%; Score 1502; DB 16;
61.3%; Pred. No. 7.4e-90;
iive 68; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimberly RP, Koopman WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU72801 standard; Protein; 464 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-2001; 2001WO-US14151.
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                                                                        282; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou T, Ichikawa K,
                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-049338/06.
   445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRA-8 heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200183560-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2001.
Sequence
                                                                                                                                                                                                                                                                 139
                                    Query Match
                                                                        Matches
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The invention describes a novel antibody which recognizes a tumour necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor (DES (Located on chromosome 8p21-22). The antibody has apoptosis-inducing activity to a cell expressing DRS in vivo. It is also useful for preparing a therapeutic for selective apoptosis of abnormal or dysregulated cells, and for inhibiting cell proliferation in a cell, preferably a human breast, ovary, colon, haematopoietic, prostate, lymphatic, lung, glioma or liver cell. A therapeutic agent may also be administered e.g. paclitaxel, taxol or cyclohaximide. The antibody is used to treat an autoimmune disease, systemic lupus cartibody is used to treat an autoimmune disease, systemic lupus cartibody. Hashimoto's disease, rheumatoid arthritis, graft-versus-host disease, soldren's syndrome, corrolmmune haemolytic anaemia, sterility, myasthenia gravis, multiple calcingmune haemolytic anaemia, sterility, myasthenia gravis, multiple collerosis, Basedow's disease, insulin-dependent diabetes mellitus, cardiomyopathy, thankel antibody and after organ and numerous malitanesias, financias of line, processed translantation and numerous malitanesias, financias of line, processed translantation and numerous malitanesias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 LEWLGVIWSGGD-TDYNAAFISRLSISKDNSKSQLFFKMNSLRATDTAIYYCARNRGDIY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 YDFTYAMDYWGQGTSVTVSSAKTTPPİSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 -DSMITTDYWGQGTTLIVSSAKTTPPSVYPLAPGSAAQINSMVTLGCLVKGYFPEPVTVT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 WNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 GPISTINPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 -----RDC-GCKPC-ICTVPEVS--|SVFIFPPFKPKDVLTITLFPKVTCVVVDISKDDP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 DVQISWFVNNVEVHTAQTQTHREDYN$TIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 IERTISKIKGLVRAPQVYILPPPRAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LGLLFCLVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibody specific for tumour necrosis factor-related apoptosis-inducing ligand, useful for inhibiting cell proliferation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplantation, and numerous malignancies of lung, prostate, liver, ovary, lymphatic or breast tissue. Peptides used to design primers for isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are shown in AAU77799 and AAU72800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 KDTAPVLDSDGSYFIYSKLNMKTSKW\pktdSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 61.1%; Pred. No. 1.5e-89;
Matches 291; Conservative 66; Mismatches 100; Indels 19;
                                                                                                                                         Claim 26; Page 198-199; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               464 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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AAR66758 standard; Protein; 465 AA.

Page 10

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Matches 282; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-1995;
                                                                                                                                                                                                                                                                                                                 25-JUN-1996
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                                                                                                                                                                                                                                RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 MDYWGQGTSVTVSSAKTIPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 SSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPISTI 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 SSGWHTFPAVLQSDLYILSSSWIVPSSPRPSETVICNVAHPASSIKVDKKIVP---- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LVTFPSCVLSQVQLKQSGPGLVQPSQSLSITCTVSGFSLTSYGVHWVRQSPGKGLEWLGV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 ILSVTSGVYSQVQLQQSGAELARPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch al Similarity 60.0%; Pred. No. 2.88-89; 282; Conservative 73; Mismatches 100; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transformed plant producing animal-derived anti-virus antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              monocional antibody. The CDNAS were incorporated into a Ti
plasmid vector, which was incorporated into A. tumefaciens.
The resultant plant expression vector was used to transform
tobacco plants, making them TWV resistant, the plants could
also be blofarmed for the prodn. of anti-virus antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chains of an animal derived anti-tobacco mosaic virus (TMV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tobacco plants producing anti-tobacco mosaic virus
                                                Anti-tobacco mosaic virus monoclonal Ab heavy chain.
                                                                                            heavy chain; virus-resistant plants; biofarming.
                                                                               Tobacco mosaic virus; TMV; monoclonal antibody;
                                                                                                                                                                                                                                      "variable heavy domain"
                                                                                                                                                                                                                                                                                          "constant heavy domain"
                                                                                                                                                                                                                                                                "J heavy 4 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Pages 14-15; 26pp; Japanese.
                                                                                                                                                                                                         /label = mat_peptide
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                               /label= leader
                                                                                                                                                                                                                                                                                                                                                                                                         93JP-0131208.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (NISB ) JAPAN TOBACCO INC. (KURS ) KURARAY CO LTD.
                         01-SEP-1995 (first entry)
                                                                                                                                                                                                                                                    ..141
                                                                                                                                                                                                                                                                                .465
                                                                                                                                                                                                                                                                   /note= '
142..469
/note= '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monoclonal antibody
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                                                                                                                                                                                                                                                                                                                          JP06319396-A.
                                                                                                                                                                                                                                                                                                                                                                               07-MAY-1993;
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                                                                                                                           Synthetic
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AAR66758;
                                                                                                                                                                    Peptide
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using insect guts, partic. insect brush border membranes (BBMs), esp. corn rootworm, as antigen; immunising a donor animal with the antigen; isolating immunocompetent B cells from the immunised animal; fusing B isolating immunocompetent B cells from the immunised animal; fusing B isolating immunocompetent B cells from the immunised animal; fusing B cells with a tumour cell line; isolating the fused cells, culturing them and cloning positive hybrid cells; and screening the hybrid cells for prodn. of the required MAbs. The MAbs bind to the gut of a target insect bind to most bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin moiety, esp. selected from e.g. Bacillus toxins, Pseudomonas exotoxin and phytolaccin, etc.. The Abs are useful for control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
                                                                                                                                                         309 FVNNVEVHTAQTQTHREDYNSTIRVVSTLPIQHQDWMSGKEFKCKVNNKDLPSPIERTIS 368
                                                                                                                                                                                                     369 KIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPV 428
                                                                                                                                                                                                                                                                                                                                                                                              356 KTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPI 415
                                        241 RDC-GCKPC-ICTVPEVS---SVFIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.2%; Score 1484; DB 17; Length 599;
60.5%; Pred. No. 1.5e.88;
tive 70; Mismatches 90; Indels 24; Gaps
249 NPCPPCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monoclonal antibodies which bind insect gut proteins - used partic. with toxin moleties for the control of insect pests, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           maize; pesticide; brush border membrane vesicle; monoclonal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 LDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               416 MNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          delta endotoxin; Bacillus thuringiensis; western corn rootworm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3B1 single chain antibody from pCIB4631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR90837 standard; Protein; 599 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-IB00497.
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KEYWO! SOURCE ORG June 23, 2003, 20:08:07; Search time 1558.31 Seconds (without alignments) 10174.698 Million cell updates/sec • • • • 32308132 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 16154066 seqs, 8097743376 residues OM nucleic - nucleic search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_gss_other:*
em_gss_pro:*
em_gss_rod:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 em_gss_pln:*
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gb_est5:* ssb_qb. EST:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AK002514 Misc misc control of the co	BCGCG371 COSSESSES	BG966302 40283024	BC031349 Mus muscu	RIA54240 603170666	BQ960162 AGENCOURT
SUMMARIES	ID	AK002514	BG969371	BG966302	BC031349	B1454240	BQ960162
	DB		13	13	11	13	14
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dР	Query	89.7	71.8	70.0	68.8	68.8	68.7
	Score	878	702.8	685.2	674.4	674	672.6
	esult No.	7	7	ო	4	2	9

	939 bp mRNA linear HTC 19-JAN-2002	Mus musculus adult male kidney cDNA, RIKEN full-length enriched	library, clone:0610010P20:immunoqlobulin kappa chain variable 28					Mus musculus (strain:C57BL/6J) adult male kidnev cDNA to mRNA.	enriched mouse cDNA library	7		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi:	Sciurognathi: Muridae: Murinae: Mus			DNA cloning	(66)				Carninci, P., Shibata, Y., Hayatsu, N., Suqahara, Y., Shibata, K.	, Muramatsu, M. and Havashizaki.v	Normalization and subtraction of cap-trapper-selected cDNAS to	aries for rapid discovery of new genes	Genome Res. 10 (10), 1617-1630 (2000)			
	AK002514 939	Mus musculus adult male kidne	library, clone:0610010P20:imn	(V28), full insert sequence.	AK002514	AK002514.1 GI:12832550	HTC; CAP trapper.	Mus musculus (strain:C57BL/6)	clone_lib:RIKEN full-length enriched mouse cDNA library	clone:0610010P20.	Mus musculus	Eukaryota; Metazoa; Chordata;	Mammalia; Eutheria; Rodentia;		Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Meth. Enzymol. 303, 19-44 (19	99279253	10349636	2	Carninci, P., Shibata, Y., Haya	Itoh, M., Konno, H., Okazaki, Y.	Normalization and subtraction	prepare full-length cDNA libr	Genome Res. 10 (10), 1617-163	20499374	11042159	_
KESULT 1 AK002514	LOCUS	DEFINITION			ACCESSION	VERSION	KEYWORDS	SOURCE			ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS		TITLE		JOURNAL	MEDLINE	PUBMED	

TITLE

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/gene="Igk-V28"
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         XhoI. Host: SOLR
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         Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoneda,Y., Inhikawa,T., Ozawa,K., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10 (11), 1757-1771 (2000)
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Encyclopedia Project of Genome Exploration Research Group in Ri
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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VYAATNLADGVPSRESGSGSGTQYSLKINSLQSEDEGSYFCQHFWGTPRTFGGGTKLE
IKRADAAPTVSIFPPSSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSW
TDQDSKDSTYSMSSTLTLITKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQGKSPQLL
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="data source:MGD, source key:MGI:96511,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.7%; Score 878; DB 11; Length 939; 96.6%; Pred. No. 4.9e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoglobulin kappa chain variable 28 (V28)
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                                                                                                          /strain="C57BL/6J"
/db_xref="FANTOM_DB:0610010P20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                         /db_xref="MGD:MGI:1900167"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="BAB22154.1"
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/db_xref="MGD:MGI:96511"
                                                                                          /organism-"Mus musculus"
                                                                                                                                                                               /db_xref="taxon:10090"
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                                                 Location/Qualifiers
                                                                                                                                                                                                      /clone="0610010P20"
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421 TCCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGC 480
                                  493 CTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGAT 552
                                                  553 TGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGGAAAGA 612
                                                                                                                        CAGCACCTACAGCATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAA 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 12-JUN-2001
                                                                                                                                                                                               673 CAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAA 732
                                                                                                                                                                                                                                                                    733 CAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAGCTCCCAGCTCCATC 792
                                                                                                                                                                                                                                                                                                                                         793 CTATCTTCCCTTCTAAGGTCTTGGAGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTG 852
                                                                                                                                                                                                                                                                                                                                                                                                                              781 CTATCTTCCCTTCTAAGGTCTTGGAGGCTTCCCCACAAGGGACCTACCACTGTTGCGGTG 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 CICCAAACCICCICCCCCCCCTICICCICCICCTCCTTICCTTGGCITTIAICAIGC 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602836854F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4971397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Plate: LLAM10956 row: k column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 ATCAACAGCCTGCAGCCTGAAGATTIJTGGGAGTTATTACTGTCAACATTTTTGGAGTACT 385
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†GCTCACTCAGGTCCTGGCGTTGCTGTGG
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Technologies. Note;
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 67 Row: j Column: 4
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon: Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 ACAGTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGCTGGCTTACAGGTGCC 97
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                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                            NIH, MGC http://mgc.nci.nth.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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Clone distribution: MGC clone distribution information can be found
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                                                                                                                                                                                                                                            757 GICCIGAGACGCCACCACCA---GCICCCCAGCICCATCCIATCITCCCTTCTAAGGICT 813
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                           518 ITCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGC 577
                                                                                                                      578 GTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACC 637
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Marcello Bento Soares, Ph.D.
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702 CATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCT 761

762 GAGACGCCACCACCTCCCCAGCTCCATCTTTCTTCTTAAGGTCTTGGAGGCT 821

642 CGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGA 701

BI454240 805 bp mRNA linear EST 21-AUG-2001 603170666F1 NCI_CGAP_Mam5 Mys musculus cDNA clone IMAGE:5250017 5', 941 Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. /note="Organ: mammaty; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators 89 ACAGGIGCCAGAIGIGACAICCAGAIGACICAGICICCCAGCCICCCIAICIGCAICIGIG 148 GGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGG 208 9 Lothar Hennighausen/Robin Humphreys, 822 ICCCCACAAGCGACCTACCACTGTT¢CGGTGCTCCAAACCTCCTCCCCACCTCCTTCTCC 882 ICCICCICCCTITCCIIGGCITTIAȚCAIGCIAAIAIIIGCAGAAAAIAIICAAIAAAGI Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be NIH-MGC http://mgc.nci.nih.gbv/. National Institutes of Health, Mammalian Gene Collection (MGC) 30 GAICACACACAGICAIGAGIGIGCICA 68.8%; Score 674; DB 13; Length 805; 94.0%; Pred. No. 1.2e-94; Indels found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM11631 row: d column: 18 /clone="IMAGE:5250017"
/clone_lib="NOI_CGAP_Mam5"
/tissue_type="tumor; gross tissue"
/dev_stage="7" months"
/lab_host="DH10B" 942 GAGTCTTTGCAAAAAAAAAAAAAAAAAAAAAAAA 977 900 GAGTCTTTGCACTTGAAAAAAAAAAAAAAAAAA 935 40; 180 t 94.0%; Pred. 4.7.+.ve 0; Mismatches Contact: Robert Strausberg, Ph.D. /organism="Mús muschlus" /db_xref="taxon:10090" High quality sequence stop: 7
Location/Qualifiers 186 g providing samples: /strain="C57BL/6J" BI454240.1 GI:15244896 209 c Unpublished (1999) Conservative mRNA sequence. house mouse. Similarity 756; Query Match Best Local source DEFINITION ORGANISM BASE COUNT RESULT 5 BI454240 ACCESSION REFERENCE JOURNAL Matches KEYWORDS FEATURES VERSION ORIGIN ŏ g δλ Ωp Qγ ъ q δλ qq δλ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 GCCCACTCACAAGACATCAACTTCACCATTGTCAAGAGCTTCAACAGGAATGAGTGTT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       747 AGAGACAAAGGTCCTGAGA--CGCCACCACCTCCCCAGCTCCATCC---TATCTTCC 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                721 AGAGACAAAGGICCIGAGAACGCCACCACCAGCICCCCAGCICCAAICCIAIICIIICC 780
                                                                                                                                                                                                                                                                                                                                                                                                                 267
                                                                                                                                                                                                                                                                                                                                                                                                                                   601 GAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          688 GG-CCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTT 746
209 TATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCA 268
                      301 AACAGCCTGCAGCCTGAAGATTTTGGGACTTATTACTGTCAACATCATAAGGGCACTCCG 360
                                                                                                                                                                                                                                                   389 TACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTA 448
                                                                                                                                                                                                                                                                     449 TCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTC 508
                                                                                                                                                                                                                                                                                                                                                    568 ACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAAAGACAGCACCTACAGCAT 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 GAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGA 687
                                                                                                                        241 GAAGGIGIGCCAICAAGGIICAGIGGCAGIGGAICAGGCACACAGIIITICICIAAAGAIC 300
                                                                                                                                                                  329 AACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                 509 TTGAAC-AACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                   269 GATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGENCOURT_8948728 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6478507 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov
Plate: LLAM14022 row: c column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            802 CTTCTAAGGTCTTGGAGGCTTCCC 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 CTTCTAAGGTCTTGGAGGCTTCCC 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ960162.1 GI:22375640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 857)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FINITION
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845 TIGCGGT-GCTCCAAACCTCCTCCCACCTCCTTCTCCTCCTCCTTT--CCTTGGC 901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  486 GAGGIGCCICAGICGIGIGCIICTIGAACAACIICTACCCCAAAGACAICAAIGICAAGI 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 GCAAAGACAGCACCTACAGCATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAAC 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      666 GACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGA 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726 GCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAGCTCCCCAG 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      786 CTCCATCCTATCTTCCCTTCTAAGGTCTTGGAGGCTTCCCCACAAGCGACCTACC-ACTG 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602 crecarecrarerrecerreraagererregaggerrececacaagegaceraceaacre 661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 GGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTG 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 GAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  546 GGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACA 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:6478507"
/clone_lib="NCI_CGAP_CG24"
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/note="Organ: colon; Vector: pCWV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCWV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCWV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCWV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: phage of the colon organization of the colon organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization organization orga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 TCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GGGCTGATGCTGCACCACCATGTATCCCACCATCCACCATCCAGTGAGATTAACATCTG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATATTAACACTTACTTAGCATGGTATCAGCAGAAAAAGGGAAAATCTCCTCAACTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 GAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                            /strain="FVB/N"
/db_xref="taxon:10090"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.78;
93.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 744; Conservative
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782 AAAAAAAAAAAA 795
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COOP #0: T#: 07

BG967689 721 bp mRNA linear EST 12-JUN-2001 602833496F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4988038 5', Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Plate: LLAM10999 row: p column: 23 Contact: Robert Strausberg, Ph.D. High quality sequence stop: 720. Location/Qualifiers BG967689.1 GI:14355326 (bases 1 to 721) Unpublished (1999) mRNA sequence. BG967689 Mus musculus house mouse. BG967689 source DEFINITION ORGANISM ACCESSION REFERENCE JOURNAL AUTHORS BG967689 KEYWORDS TITLE EATURES VERSION COMMENT SOURCE LOCUS

/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by.Life
Technologies. Note: this is a NCI_CGAP Library."
a 176 c 168 g 165 t /organism="Mus musculus" /db_xref="taxon:10090" /clone="IMAGE:4988038" /strain="FVB/N"

212 a

ASE COUNT

RIGIN

24 CACACTGATCACACACAGTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGTTGT 0; Gaps h 68.3%; Score 668.2; DB 13; Length 721; Similarity 95.4%; Pred. No. 1e-93; 88; Conservative 0; Mismatches 33; Indels 0; 688; Conservative Query Match Best Local Matches

GGCTTACAGGTGCCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCAT 143

264 TAGCAGATGGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCA 323

324 AGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTA 383

384 CICCGIACACGIICGGAGGGGGGAC¢AAGCIGGAAAIAAAACGGGCIGAIGCIGCACCAA 443 503 504 GCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTG 563 564 AACGACAAAATGGCGTCCTGAACAGI|TGGACTGATCAGGACAGCAAAAGACAGCACCTACA 623 624 GCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTATGAACGACATAAACAGCTATACCT 683 684 GTGAGGCCACTCACAAGACATCAACTITCACCCATTGTCAAGAGCTTCAACAGGAATGAGT 743 444 CIGIATCCATCTTCCCACCATCCAGGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGT 744 G 744 q δλ g QΥ qq δλ qq ŏ g ò pp ò

EST 21-AUG-2002 BQ956722 871 bp mRNA linear EST AGENCOURT_8880991 NCI_CGAP_CD24 Mus musculus cDNA clone IMAGE:6396481 5', mRNA sequence. BQ956722 BQ956722 DEFINITION ACCESSION RESULT 8 BQ956722

BQ956722.1 GI:22372200 house mouse. ORGANISM KEYWORDS VERSION

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. Mus musculus Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia (bases 1 to 871) REFERENCE AUTHORS

NIH-MGC http://mgc.ncl.nih.gbv/. National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, ph.D. Unpublished (1999) TOURNAL

TITLE COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov n column: 02 Email: cgapbs-remail nih gov Tissue Procurement: The Cepko Laboratory CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation

Location/Qualifiers High quality sequence stop: Source

FEATURES

/organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090"

/clone_lib="NCI CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Vorgan: Colond" Vector: pCMV-SPORT6; Site_1: NotI:
/note="Vorgan: Colond unidirectionally." Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library." /clone="IMAGE:6396481"

193 t

182 g

BASE COUNT

65.4%; Score 640; DB 14; Length 871; 90.6%; Pred. No. 2e-89; Pred. Np. 2e-89; Best Local Similarity Query Match

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Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                      /strain="FVB/N"
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                                                                                                                                                                                                                  . 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737 AATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAGCTCCCAGCTCCATCTAT 796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 ACCTACAGCATGAGCACCACCTCACATTGACCAAGGACGAGTATGAACGACATAACAGC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 AATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAGCTCCCAGCTCCTAT 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            677 IATACCIGIGAGGCCACICACAAGACAICAACIICACCAIIGICAAGAGCIICAACAGG 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                    257 AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATAT 316
                                                                                                                                                                                                                    317 TCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTT 376
                                                                                                                                                                                                                                           181 CAGCGTTCCCCGTACACGTTCGGAGGGGGGACCAAGCTGGAATAAAACGGGCTGATGCT 240
                                                                                                                                                                                                                                                                                                                                                                                       437 GCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCA 496
                                                                                                                                                                                                                                                                                                                                                                                                                             241 GCACCAACTGTATCCATCTTCCCACCATCAGTGAGCAGTTAACATCTGGAGGTGCCTCA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        497 GICGIGIGCIICTIGAACAACTICTACCCCAAAGACAICAAIGICAAGIGGAAGAIIGAI 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GICGIGIGCITCITGAACAACITCIACCCCAAAGACAICAAIGICAAGIGGAAGAIIGAI 360
                                                 197 TATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCA 256
                                                                                                                                                                           61 TCCAACCTGGCTTCTGGAGTCCCAACTCGCTTCAGTGGCAGTGGGTCTGGGACCTCCTAT 120
                                                                                          1 raciigcacigciaccagcagaagccaggaicciccccaaaciciggaiitalagcaca 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF687485 944 bp mRNA linear EST 22-DEC-20
602102475F1 NCI_CGAP_Kidl4 Mus musculus CDNA clone IMAGE:4220563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            557 GGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGC
                                                                                                                                                                                                                                                                                                         377 TGGAGTACTCCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCT
               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      917 ATTTGCAGAAATATTCAATAAAGTGAGTCTTT 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 ATTIGCAGAAATATICAATANAGIGAGICTIT 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF687485.1 GI:11972893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                     Matches 682; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
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National Institutes of Health, Mammalian Gene Collection (MGC)

NIH-MGC http://mgc.nci.nih.gov/.

(bases 1 to 944)

EFERENCE AUTHORS

ORGANISM

EYWORDS

ERSION

SFINITION

ESULT 9 F687485

CESSION

Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov

Unpublished (1999)

JOURNAL

OMMENT

TITLE

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421 Grecisaacagriegacigareagacageaaagacageaceracageargageacacec 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 TCCTGAGACGCCACCACCACCTCCCAGCTCCTATCTTCCCTTCTAAGGTCTTGGA 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     818 GGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCCCACCTCCTT 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 578 GTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACC 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                638 CTCACGTIGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCAC 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 CCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGTCTTGAACAAC 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 CCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGTTCTTGAACAAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAAGGACAAAATGGC 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 CAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398 GGAGGGGGGCCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTC 457
                                                                                                                                                                                                                                                                                                                         /clone_"IMAGE:4220563"
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 GTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 CCATCAAGGITCAGIGGCAGIGGAICAGGAACACAATAIICTCTCAAAGAICAACAGCIG 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTCACCATCACATGTCGAGCAAGTGGGAATATTCACGATTATTTAACATGGTATCAGCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       541 AAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 ACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTG
                                                DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12; Length 944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.1%; Score 637.2; DB 1:
90.9%; Pred. No. 5.1e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                     http://image.llnl.gov
plate: LLAM9804 row: f column: 20
                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                    High quality sequence stop: 751.
                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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DEFINITION

ACCESSION

KEYWORDS

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BQ943305

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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277 GCCATCAAGGTTCAGTGGCAGTGGAJTCAGGAACACAATATTCTTCAAGATCAACAGCCT 336
                                                                             247 CCCTCAAGGTTCAGTGGCAGTGGATCTGGGCAAGATTATTCTCTCACCATCAACAGCCT 306
                                                                                                                         337 GCAGCCIGAAGAITITIGGGAGITAATAACTGICAACATITITIGGAGTACICCGTACACGIT 396
                                                                                                                                                 397 CGCAGGGGGGCCCAAGCTGGAAATAAAACGGGCTGATGCTGCACCCAACTGTATCCATCTT 456
                                                                                                                                                                                                                                     457 CCCACCATCCAGTGAGCAGTTAACAPCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAA 516
                                                                                                                                                                                                                                                                                                                       517 CTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAAATGG 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         577 CGTCCTGAACAGTTGGACTGATCAG¢ACAGCAAAGACAGCACCTACAGCATGAGCAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     727 GICCIGAGACGCCACCACCACCACCICCACCICATCTTCCCTTCTAAGGTCTTGG 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           817 AGGCTTCCCCACAAGCGACCTACCA¢TGTTGCGG--TGCTCCAAACCTCCTCCCCACCTC 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG518527 874 bp mRNA linear EST 02-APR-200
602578261F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491798 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697 CAAGACATCAACTTCACCCATTGTCÅAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         757 GICCIGAGACGCCACCACCAGGICCÁCAGCICCAICCIAICTICCCIICIAAGGICIIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gpv/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               875 C-TTCTCCTCCTCCTCCC--TTTCCTGGGCTTTTATCATGCTAATATT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM8536 row: i column: 15
High quality sequence stop: 843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Rodentia;
1 (bases 1 to 874)
                                                                                                                                                                                                                                   BG518527.1 GI:13513491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
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JOURNAL
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878 CICCICCICCTCCTTTCCTTGGCTTTTATCATGCTAATATTTGCAGAAAATATTCAATA 937
                                                                                                       715 TCTCTCTCTCTTTCTT-----GGGTTTATCATGCTATATTTGCGAAATATTCATAAAGT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 CANATGIGACAICAAGAIGACCCAGICICCAICIICCAIGIAIGCAICITAAGGAGGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 TGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTAGCATGGTATCAGCA 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 GGTCACTATCACTTGCAAGGCGAGTCAGGACATTTATTCCTATTTAAAATGGTTCCAGCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 GACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 CACAGTCATGAGTGTGCTCACGTCCTGGCGTTGCTGCTGCTGTGGCTTACAGGTGC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGACATGAGGACCCCTGCTCAGTTTCTTGGAATCTTGTTGCTCTTGGTTTCCAGGTGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:6397142"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_8880809 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6397142 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 65.0%; Score 636.8; DB 14; Length 901; Similarity 84.5%; Pred. No. 6e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 133; Indels
                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.linl.gov
Plate: LLAM13894 row: i column: 15
High quality sequence stop: 670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                            BQ943305.1 GI:22358783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse.
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756

816

EST 02-APR-2001

Query Match

ASE COUNT

Best Local

Matches

93

ATURES

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                               VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 CGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCAC 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          697 CAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 GCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 GCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 GGAGTCTGACGATACAGCAACTTATTACTGTCTACAGCATGGTGAGGCCCGTATACGTT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 CGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTT 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           388 CGGATCGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 CCCACCATCCAGIGAGCAGTIAACATCTGGAGGTGCCTCAGTCGTGGTGCTTCTTGAACAA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 GACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGGTGT 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 CCCATCAAGATTCAGTGGCAGTGGGTCTGGGCAAGATTATTCTCTAACCATCAGCAGCGT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 TGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCA 216
                                                                                                                                                                                                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 CAGATGIGACAICCAGAIGACTCAGICICCAGCCICCCIAICTGCAICIGIGGGAGAAAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 CAGATGTGACATCAAGATGACCCAGTCTCCATCCTCCATGTATGCATCGCTGGGAGAGAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AGTCACTATCACTTGCAAGGCGAGTCAGGACATTAAAAGCTATTTAAGCTGGTACCAGCA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 CACAGTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGCTGTGGCTTACAGGTGC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CATGGACATGAGGGCCCCTGCTCAGTTTTTGGGATCTTGTTGCTCTGGTTTCCAGGTAT 87
                                                                                                                                            /tissue_type="spontaneous tumor, metastatic to mammary. Stem cell origin."
                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64.1%; Score 628; DB 12; Length 874; 84.6%; Pred. No. 1.4e-87; tive 0; Mismatches 130; Indels
                                                                                                                        /clone_lib="NCI_CGAP_Lu29"
                                         /orqanism="Mus musculus"
                                                                               /db_xref-"taxon:10090"
                                                                                                     /clone="IMAGE:3491798"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                  205 g
                                                           /strain="C2ECH II"
                                                                                                                                                                                          /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                    232 c
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BE162625
60170220F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3989537 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 GTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 AGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACT 157
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817 AGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCCCACCTCCT 876
                        38 ACAGTCATGAGTGCTCACTCAGGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . /tissue_type="spontaneous tumor, metastatic to mammary.
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Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Glibert Emith, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.4%; Score 620.8; DB 12; Length 950; 95.0%; Pred. No. 1.7e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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High quality sequence stop: 790.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
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                                                                                                     877 TCTCCTCC 884
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337 GCAGCCIGAAGAITITGGGAGTTAITACTGICAACAITITITGGAGTACTCCGTACACGTT 396
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                                                                                                                                                                                                          CCCACCATCCAGIGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAA 516
                                                                                                                                                                                                                                                                                                  517 CTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGG 576
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthería; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Plate: LLAM11100 row: a column: 05
High quality sequence stop: 769.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:5036044"
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CESSION

EYWORDS

ERSION

SFERENCE AUTHORS

TITLE

ATURES

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188 ATTCAAAATTATTAGCATGGTATCAGCACACAGGGAAAATCTCCTCAGCTCCTGGTC 247
                                                                                                                                                248 IATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGA 307
                                                                                                                                                            308 ACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGT 367
                                                                                                                                                                                                             368 CAACATTTTGGAGTACTCCGTACACĠTTCGGAGGGGGCCCAAGCTĠGAAATAAAACGG 427
                                                                                                                                                                                                                                                              428 GCTGATGCTGCACCAACTGTATCCAT¢TTCCCACCATCCAGTGAGCAGTTAACATCTGGA 487
                                                                                                                                                                                                                                                                                                              488 GGTGCCTCAGTCGTGCTTCTTGAA¢AACTTCTACCCCAAAGACATCAATGTCAAGTGG 547
                                                                                                                                                                                                                                                                                                                                                               EST 26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      728 ITCAACAGGAATGAGTGTTAGAGACAÅAGGTCCTGAGACGCCACCACCAGCTCCCCAGCT 787
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                                                                         94; Indels
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Gilbert Smith, NIH'
                                                Score 618.6; DB
Pred. No. 4e-86;
0; Mismatches 9
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providing samples:
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                                               63.2%;
87.8%;
          230 c
                                                                     Matches 686; Conservative
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BI100311
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          212 a
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                                               Query Match
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          BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             764 GACGCCACCACCACCTCCCAGCTCCATCTTCCCTTCTAAGGTCTTGGAGGCTTC 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 AACAGTIGGACTGATCAGGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCTCACG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        644 ITGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 GGITCAGIGGCAGIGGAICAGGAACACAATAI-TCICTCAAAATCAACAGCCIGCAGCCI 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344 GAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464 TCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTGGTGTTCTTGAACAACTTCTAC 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 TCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTAC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 GAAGACCIGGCAGITTAITACIGICAGCAATATIATAGCIATCCICCCACGIICGGAGGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATTTCCCACCA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 gcrrcacagecegregarcregaacagearrrcacrercacaarcageagegrefea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_libb="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |
199 c 152 g 160 t
                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Trissue Procurement: Jeffrey E. Green, M.D.
CDN Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.1%; Score 607.6; DB 13; Length 712; 93.5%; Pred. No. 2.1e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 44; Indels
                                                                                                                                                                                                                                                                                                                                                                   Plate: LLAM11113 row: g column: 19
High quality sequence stop: 680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:5041194"
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                                                                                   (bases 1 to 712)
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                                                                                                                                                  Unpublished (1999)
                      Mus musculus
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house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602833891F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988182 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 AGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCG 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 196 c 148 g 162 t
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                                                                                                               884 CICCICCTITCCIIGCCITITAICAIGCIAATAITIGCAGAAAAIAITCAATAAAGIGA 943
                                                                                                                                                                       605 CICCICCITICCITGGCITITATCATGCTAATATITGCAGAAAATATTCAATAAAGTGA 664
824 CCCACAAGCGACCTACCACTGTTGCGGTGCTCCTCCTCCTCCCCACCTCCTTCTCCTC 883
                                                       545 CCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCCCACCTCCTTCTCTC 604
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.f column: 23
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                        944 GTCTTTGCAAAAAAAAAAAAAAAAAAAAA 973
                                                                                                                                                                                                                                                                                                665 GTCTTTGCACTTGAAAAGAGACAAGAGAA 694
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/db_xref="taxon:10090"
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BG967208
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qq	241 TCTACCCCAAAGACATCAAAGACAACAAACAACAACAACAACAACAACAACAAACAAC

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CCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACAGCACCACAGCATGAGAGCACAGCAAAGACAGCACCTACAGCATGAGCAGCACCG 360

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639 TCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACA 698

699 AGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGT 758

759 CCTGAGACGCCACCACCTCCCCAGCTCCCATCCTATCTTCCCTAAGGTCTTGGAG 818

939 AGTGAGTCTTTGCAAAAAAAAAAAAAAAAAAAAAAAAA 979

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OM nucleic - nucleic search, using sw model

June 23, 2003, 20:29:16 ; Search time 779.157 Seconds Run on:

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US-09-770-916-3 Perfect score:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Sequence:

Title:

7820798 seqs, 3482471992 residues Searched:

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4inimum DB seq length: 0 4aximum DB seq length: 2000000000

Potal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

	Description		Sequence 3410, Ap	Sequence 12/85, A	Seguence 143/3, A	Sociono 12710 3	Sequence 12/10, A	Socionos (FEEE)	Segmence 03009, A	7 0	Sequence 22, Appl		€	Sequence 22, Appl		ì	_	Sequence 79, Appl	Sequence 125, App		4	<u>,</u>	Sequence 183, App
SOMMAKIES	OI 1	0 HS-10-210-0618-2410	0 HS-10-219-04E0	0 US-10-219-051B 12/83	US-10-144-771-21147	0 US-10-219-051B-12710	US-10-236-051-7	0 US-10-424-599-65669	PCT-US02-34420A-22	PCT-US02-35333A-22	US-10-286-1328-22	US-10-281-470A-22	0 HS-10-275-1803-22	TIS-09-726-2198-	0 HS-10-384-033-10	IIS-10-251-215-47	75-10-450 11-20	6/-41/-628-11-60	PCT-US03-01096-125	US-10-236-051-3	US-10-458-714-81	0 110-406-011	0 03-10-403-02/-183
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21 420.2 42.9 941 10 22 405.2 41.4 631 10 24 403.2 41.4 729 10 25 40.3 41.2 621 10 26 394.6 40.3 705 1 27 394.6 40.3 705 1 29 394.6 40.2 6082 1 30 393.6 40.2 6082 1 31 392.2 40.1 1161 1 32 392.2 40.1 1161 1 34 392.2 40.1 1161 1 35 392.2 40.1 1161 1 36 391.6 40.0 632 1 37 389.8 39.8 708 1 40 389.8 39.8 708 1 40 389.8 39.6 6082 1 41 387.6 39.6 6082 1 44 387.6 39.6 6082 1 45 387.6 39.6 6082 1 46 387.6 39.6 6082 1	405-027-1446 398-104-281 384-933-125 398-104-283 1-170-235-39856 22-36107-47 292-088-47	395-894-10 398-104-287 776-781-108 33-03134-2996 219-051B-14371 436-643-2996 398-104-285 06-276A-3 292-088-23 292-088-23 401-344-3 2-33944-8	2-33944-9 395-894-8 395-894-9 3-03194-2997
21 420.2 42.9 941 10 22 405.2 41.4 631 10 24 403.2 41.4 729 10 25 40.3 41.2 621 10 26 394.6 40.3 705 1 27 394.6 40.3 705 1 29 394.6 40.2 6082 1 30 393.6 40.2 6082 1 31 392.2 40.1 1161 1 32 392.2 40.1 1161 1 34 392.2 40.1 1161 1 35 392.2 40.1 1161 1 36 391.6 40.0 632 1 37 389.8 39.8 708 1 40 389.8 39.8 708 1 40 389.8 39.6 6082 1 41 387.6 39.6 6082 1 44 387.6 39.6 6082 1 45 387.6 39.6 6082 1 46 387.6 39.6 6082 1	US-10 US-10 US-10 US-10 US-10 PCT-US	US-10- US-10- US-10- PCT-USC US-00- US-09-E US-09-E US-09-E US-10- US-10- US-10- US-10- US-10-	PCT-USC US-10- US-10- PCT-USO
21 420.2 42.9 24 405.2 41.4 24 403.2 41.4 25 394.6 40.3 27 394.6 40.3 28 394.6 40.3 39.6 40.3 39.6 40.2 39.8 40.2 39.8 40.1 39.2 40.1 39.2 2 40.1 39.2 2 40.1 39.8 39.8 39.8 39.8 39.8 39.8 40.8 39.8 40.8 39.8 40.8 39.8 41.8 387.6 39.6 44.3 387.6 39.6 45.8 39.6 46.3 387.6 39.6 46.3 387.6 39.6	100000000000000000000000000000000000000		1001
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ALIGNMENTS

RESULT 1 US-10-219-051B-3410 Sequence 3410, Ap. Sequence 3410, Ap. Sequence 3410, Ap. TITLE OF INVENTI FILE REFERENCE: CURRENT FILING DAT CURRENT FILING DAT PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO PRIOR APPLICATIO SEQ ID NO 3410 LENGTH: 998 TYPE: DNA TYPE: DNA CORGANISM: HOMO SA	SGULT 1 -:10-219-051B-3410 Sequence 3410, Application US/10219051B Sequence 3410, Application US/10219051B Sequence 3410, Application US/10219051B APPLICANT: The General Hospital Corporation doing business as Massachusetts Genera APPLICANT: Hospital / Bayer AG TITLE OF INVENTION: Nucleotide Sequences Involved in pain FILE REFERENCE: LeA 35693 Foreign Countries CURRENT APPLICATION NUMBER: US/10/219,051B PRIOR APPLICATION NUMBER: US 60/312,147 PRIOR APPLICATION NUMBER: US 60/346,382 PRIOR APPLICATION NUMBER: US 60/346,382 PRIOR APPLICATION NUMBER: US 60/346,382 PRIOR APPLICATION NUMBER: US 60/333,347 PRIOR APPLICATION NUMBER: US 60/333,347 PRIOR APPLICATION SEC 1D NOS: 14715 SEQ ID NO 3410 LENGTH: 998 TYPE: DNA ORGANISM: HOMO sapiens ORGANISM: TURNAMENTON TURNAMENTO
; DATABASE ACCESS; DATABASE ENTRY; DATABASE ENTRY; US-10-219-051B-3410	FOBLICATION IN FORMATION: DATABASE ACCESSION NUMBER: EMBL / S65921 DATABASE ENTRY DATE: 2000-03-04 10-219-051B-3410
Query Match	Query Match 74.9%; Score 733.6; DB 10; Length 998;
Best Local	Best Local Similarity 87.6%; Pred. No. 1.3e-129;
Matches 80	Matches 802; Conservative 0; Mismatches 114; Indels 0; Gaps 0;
Qy	37 CACAGTCATGAGTGTGCTCAGTCAGGGGTTGCTGCTGCTGTGGCTTACAGGTGC 96
Db	
Qy	97 CAGATGTGACATCCAGATGACTCAGTCTCCCTATCTGCATCTGTGGGAGAAAC 156
Db 1	
Qy 1	157 TGTCACCATCACATGTCGAGCAAGTGGGAATATTTCAAAATTATTTAGCATGGTATCAGCA 216
Db 1	

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697 CAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
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                                                                                                                        74.9%; Score 733.6; DB 10; Length 998;
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                                                                                                                                         Pred. No. 1.3e-129;
                                PUBLICATION INFORMÁTION:
DATABASE ACCESSION NUMBER: EMBL / S65921
DATABASE ENTRY DATE: 2000-03-04
                                                                                                                                             87.6%;
                                                                                                                                                                Matches 802; Conservative
                   ORGANISM: Homo sapiens
                                                                                                                                               Best Local Similarity
                                                                                       US-10-219-051B-12785
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                                                                          277 GCCATCAAGGIICAGIGGCAGIGGAICAGGAACACAAIAIICICICAAAGAICAACAAGCI 336
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217 GACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGT
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                                                                                                                319 CCCATCAAGGTTCAGTGGCAGTGGATCTGGGCAAGATTATTCTCTCACCATCAGCAGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleotide sequences involved in pain FILE REFERENCE: LeA 35693 Foreign Countries CURRENT APPLICATION NUMBER: US/10/219,051B CURRENT FILING DATE: 2003-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/312,147
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877 TCTCCTCCTCCTTCCCTTTCCTTGGCTTTTATCATGCTAATATTTGCAGAAAATATTCAAT 936

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PRIOR FILING DATE: 2001-11-01 PRIOR APPLICATION NUMBER: US 60/333,347 PRIOR FILING DATE: 2001-11-26

SSULT

NUMBER OF SEQ ID NOS: 14715 SOFTWARE: Perl script

SEQ ID NO 12785 LENGTH: 998

937 AAAGTGAGTCTTTGCA 952

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7007 CO:T#:07 T

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; Sequence 21147, Application US/10144771
; GENERAL INFORMATION:
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US-10-144-771-21147
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LENGTH: 2221
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                                                             APPLICANT: The General Hospital Corporation doing business as Massachusetts General
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Past Local Similarity 87.6%; Pred. No. 1.3e-129;

Matches 802; Conservative 0; Mismatches 114; Indels 0;
                                                                             TITLE OF INVENTION: Nucleotide sequences involved in pain FILE OF INVENTION: Nucleotide sequences involved in pain FILE OF INVENTION: Nucleotide sequences involved in pain FILE REFERENCE: LeA 5569 Foreign Countries CURRENT APPLICATION NUMBER: US/10/219,051B CURRENT FILING DATE: 2003-05-09 PRIOR PELICATION NUMBER: US 60/312,147 PRIOR APPLICATION NUMBER: US 60/3146,382 PRIOR FILING DATE: 2001-11-01 PRIOR APPLICATION NUMBER: US 60/333,347 PRIOR FILING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 14715
                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: EMBL / S65921
DATABASE ENTRY DATE: 2000-03-04
                         Sequence 14373, Application US/10219051B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
     JS-10-219-051B-14373
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1304 TGTCTCTAGGGCAGAGAGACCACATCTCCTGCAGAGCCAGTGAAAGTGTTGAATATTATG 1363
                          CAAGACATCAACTTCACCCATTGTCÅAGAGCTTCAACAGGAATGAGTGTTAAGAGACAAAG 756
                                                                                                                    GTCCTGAGACGCCACCACCAGCTCC¢CAGCTCCATCCTATCTTCCCTTCTAAGGTCTTGG 816
                                                                                                                                                                                                            1604 TCGGTGGAGGCACCAAGCTGGAAATCAAAACATTCACGTTCGGCTCGGGGACAAAGTTGGA 1663
CCTCACGTTGACCAAGGACGAGTAT¢AACGACATAACAGCTATACCTGTGAGGCCACTCA 696
                                                                                                                                                                                                                                                                               817 AGGCITCCCCACAAGGGACCTACCA¢TGTTGCGGTGCTCCAAACCTCCTCCCCACCTCCT 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 TGTGGCTTACAGGTGCCAGATGTGACATGACTCAGATCTCCAGCCTCCCTATCTG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 CATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 ATTCTGCAAAAACCTTAGCAGATGGT¢TGCCATCAAGGTTCAGTGGCAGTGGATCAGGAA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 CACAATAITCICICAAGAICAACAGC¢IGCAGCCIGAAGAITITGGGAGITAITACTGIC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --CGTACACGTTCGGAGGGGGGACCAAGCTGGA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.9%; Score 576.6; DB 9; Length 2221; 77.8%; Pred. No. 7.2e-100; tive 0; Mishatches 134; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CLOO1321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
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44 ATGAGTGTGCTCACTCAGTCCTGGCGTTGCTGCTGCTGGCTTACAGGTGCCAGATGT 103

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869 CACCTCCTTCTCCTCCTCCTCCTTTCCTTTTATCATGCTAATATTTGCAGAAAA 928
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                                                                                                                                                                                                                                                                                        269 GAIGGIGIGCCAICAAGGIICAGIGGCAGIGGAICAGGAACACAAIAIICTCICAAGAIC 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               738 ACCCAAAGGTCCTGAGGTG---CCACCTGCTCCCAGCTCCTTCCAATCTTCCCTCAA 794
                                                                                                                                                                   138 ATATCTTGCAAGTCAAGTCAGAGCCTCGTAGGTACTAATGGAAAGACATATTTGAATTGG 197
                                                                                                                                                                                                            209 TATCAGCAGACACAGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCA 268
                                                                                                                                                                                                                                                   258 TCTGGGATTCCTGATAGGTTCAGTGGCAGTGGATCAGAGACAGATTTTACTCTTAAAATC 317
                                                                                                                                                                                                                                                                                                                                                                                                    104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACC 163
                                                                      18 ATGATGAGTCCTGCCCAGTTCCTGTTTCTGCTAATGCTCTGGATTCAGGAAACCAGTGGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/10236051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MORIARTY, Ann M.
ULEVITCH, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LETURCQ, Didier J.
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                                                                                                                                                                                                                                                                                                                                              1964 TGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAG 2023
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                    1664 AATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTT 1723
                                                                                                                     1724 AACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAA 1783
                                                                                                                                                                                                                                                                838 ACCACTGTTGCGGTGCTCCAAACCTCCTCCTCCTTCTTCTCCTCCTCCTTTCCT 897
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                                                                                                                                                                                                                                           598 TCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGA 657
                                                                                                                                                                                                                                                                                                                         GTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCAT 717
                                                                                478 AACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAA 537
                                                                                                                                                            TGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGA 597
418 AATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTT 477
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Pred. No. 5e-90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleotide sequences involved in pain FILE REFERENCE: LeA 35693 Foreign Countries CURRENT APPLICATION NUMBER: US/10/219,051B CURRENT FILING DATE: 2003-05-09 PRIOR APPLICATION NUMBER: US 60/312,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DATABASE ACCESSION NUMBER: EMBL / L22655
DATABASE ENTRY DATE: 2000-03-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILLING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
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Best Local Similarity 75.3%;
Matches 716; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hospital /
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With FILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILLE REFRENCE: 38-21(53233)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 65669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 GIGACAICCAGAIGACICAGICTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 CTATGAGCTGCAAGTCCAGATCTTTATGGATTGGAAATCAAAGGAGCTGTTTAG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 AACGACGAGATGGTGTCCTGGACAGTGTTACTGATCAGGACAGCAAAGACAGCACGTACA 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.2%; Score 471.4; DB 10; Length 870;
75.8%; Pred. No. 6e-80;
Live 0; Mismatches 181; Indels 29; Gaps
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                601 CCCATTGTCAAGAGCTTCAACAGGAATGAGTGT 633
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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                                                                                                                                                                                                                                                    Cao Yongwei
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                                                                                                            US-10-424-599-65669
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APPLICANT: TOBIAS, Peter S.
APPLICANT: MATHISON, John C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
FILE REFERENCE: SCRIPI140-4
CURRENT APPLICATION NUMBER: US/10/236,051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 CCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GTTAAAGTCCTAATCTACTACATCAAGATTACACTCAGGAGTCCCATCAAGGTTCAGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 GGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 GGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 CTGGAAATAAAACGGGCTGATGCTGCACCCAACTGTATCCATCTTCCCACCATCCAGTGAG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CAGTTAACATCTGGGGGTGCCTCAGTGGTGCTTCTTGAACAACTTCTACCCCAAAGAC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473 CAGTTAACATCTGGAGGTGCCTCAGTCGTGTTCTTGAACAACTTCTACCCCAAAGAC 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 ATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAAATGGCGTCCTGAACAGTTGG 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1)..(633)
OTHER INFORMATION: CDR1=Nucleic acids 61-93; CDR2=Nucleic acids 139-159;
OTHER INFORMATION: CDR3=Nucleic acids 256-28
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                                                                                                            CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: US 09/170,769
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/373,297
PRIOR FILING DATE: 1995-01-23
PRIOR FILING DATE: 1994-05-27
PRIOR APPLICATION NUMBER: US 08/070,160
PRIOR FILING DATE: 1994-05-28
NUMBER OF SEQ ID NOS: 26
SOFTWARRE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 633
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                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                  CYPE: DNA
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Best Local 8
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SULT 8

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APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APPORTS.
FILE REFERENCE: 21085.0029P2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  497 GTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGAT 556
                                                                                                                                                                                                                                                                                  557 GGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGC 616
                                                                                                                                                                                                                                                                                                                                                                                                       514 GCCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGC 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                     617 ACCTACAGCATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGC 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           377 IGGAGIACTCCGTACACGITCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCT 436
                                                                                          437 GCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCA 496
                                                                                                                                                                                      394 GCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCA 453
277 ACTCTCACCATTAGCAATGTGCAGTCTGAAGACTTGGCAGATATTTCTGTCAGCAATAT 336
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0; Mismatches 121; Indels 3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:/Note = OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: PCT/US02/35333A CURRENT FILING DATE: 2002-11-01
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PRIOR FILING DATE: 2001-11-01
PRIOR PELICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
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LENGTH: 705
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APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS FACTOR-
TITLE OF INVENTION: APOPPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERAPEUTIC AGENTS
FILE REPERENCE: 21085.0029P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:/Note - Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 TCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAAT 196
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                                                                                                                                   804 TCTAAGGTCTTGGAGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTC 863
                                                                                                                                                                                                         CTCCCCACCTCCTTCTCCTCCTCCTTTCCTTGGCTTTTATCATGCTAATATTTGCA 923
              744 GITAGAGACAAAGGICCIGAGACGCCACCAGCICCCCAGCICCATCTATCTICCCI 803
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                                                                                                                                                                                                                                                                                                        924 GAAAATATTCAATAAAGTGAGTCTTTGCA 952
                                                                                                                                                                                                                                                                                                                                                       837 GAATAT-TAAATAAAGGTGAATCTTTGCA 864
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CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
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PRIOR FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22, Application PC/TUS0234420A SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The UAB Research Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: IChikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oshumi, Jun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Zhou, Tong
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LENGTH: 705
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197 TATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCA 256
                                                 257 AAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATAT 316
                                                                                                             217 rccaccegeracresagrecersarcserreacasserresesses 276
                                                                                                                                     317 TCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTT 376
                                                                                                                                                   377 TGGAGTACTCCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCT 436
                                                                                                                                                                                                                                           437 GCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCA 496
                                                                                                                                                                                                                                                                                                                                             GTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGAT 556
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APPLICANT: Koopman, William J.
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN APTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APOPTOSIS-INDUCING LIGANN PERCEDANCE AND TITLE OF INVENTION: APOPTOSIS-INDUCING LIGANN PERCEDANCE. APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF Sequence 22, Application US/10286132A GENERAL INFORMATION: APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P. S-10-286-132A-22

FILE REFERENCE: 21085.0029U7
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR PLING DATE: 2000-05-02

NUMBER OF SEQ ID NOS: 102 SOFTWARE: PatentIn version 3.0

ORGANISM: artificial sequence SEQ ID NO 22 LENGTH: 705 TYPE: DNA

OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct S-10-286-132A-22 FEATURE:

77 CIGCIGIGGCITACAGGIGCCAGAI¢IGACAICCAGAIGACICAGICICCAGCCICCCIA 136 137 TCTGCATCTGTGGGAGAAACTGTCA¢CATCACATGTCGAGCAAGTGGGAATATTCAAAAT 196 257 AAAACCTTAGCAGATGGTGTGCCAT¢AAGGTTCAGTGGCAGTGGATCAGGAACACAATAT 316 317 TCTCTCAAGATCAACAGCCTGCAGCQTGAAGATTTTGGGAGTTATTACTGTCAACATTTT 376 377 TGGAGTACTCCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCT 436 GCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCA 496 557 GGCAGTGAACGACAAAATGGCGTCCTBAACAGTTGGACTGATCAGGACAGCAAAGACAGC 616 617 ACCIACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGC 676 677 TATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGG 736 GTCGTGTGCCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGAT 556 197 TATTTAGCATGGTATCAGCAGACACÅGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCA Gaps ω ,, 47.1%; Score 461.4; DB 9; Length 705; 81.5%; Pred. No. 4.7e-78; tive 0; Mismatches 121; Indels Best Local Similarity o...
Matches 547; Conservative 737 AATGAGTGTTA 747 Query Match 497 δy g ò q οy g ò g δ QQ à g ò q ò qq ŏ qq à ò g Ω

APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchabaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T APPLICANT: The UAB Research Foundation Sequence 22, Application US/10281479A GENERAL INFORMATION: APPLICANT: Koopman, William J. APPLICANT: Oshumi, Jun APPLICANT: Ichikawa, Kimihisa APPLICANT: Kimberly, Robert P. Zhou, Tong US-10-281-479A-22 APPLICANT:

CURRENT APPLICATION NUMBER: US/10/281,479A CURRENT FILING DATE: 2003-01-28 CURRENT FILING DATE: 2003-01-28 PRIOR APPLICATION NUMBER: 60/391,478 FILE REFERENCE: 21085.0029U6

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APPLICANT: KOOPMEN, William J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOP
TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029U5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    677 TATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGG 736
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                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:/Note OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/275,180A CURRENT FILING DATE: 2002-10-31
                 APPLICANT: The UAB Research Foundation
                                     Zhou, Tong
Ichikawa, Kimihisa
Kimberly, Robert P.
                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-10-3
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 547; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           705
                                                                                                                                                                                                                                                                                                                     SEO ID NO 22
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                            APPLICANT:
                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 GCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCA 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR PLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
                                                                                                                                                      PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       737 AATGAGTGTTA 747
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                                                                                                                                                                                                                                   SEQ ID NO 22
LENGTH: 705
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Sequence 22, Application US/10275180A

-10-275-180A-22

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1413 CTGAGCAAAGCAGACTACGAGAAAGACAAAAGTCTACGCGTGCGAAGTCACCCATCAGGGC 1472
344 GAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGG 403
                                                                                     404 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA 463
                                                                                                                                                                         464 TCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTGGTGTGTGCTTCTTGAACAACTTCTAC 523
                                                                                                                                                                                                                                                           524 CCCAAAGACATCAAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAAATGGCGTCCTG 583
                                                                                                                                                                                                                                                                                                                                              584 AACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACG 643
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79.0%; Pred. No. 3e-75;
tive 0; Mismatches 134; Indels 12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        704 TCAACTTCACCCATTGTCAAGAGCT‡CAACAGGAATGAGTGTTAGAGACAA 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
FILE REPERBNE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/10/384, 933
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499, 662
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; GENERAL INFORMATION:
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Nakahara, Kaori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Serizawa, Nobufusa
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SEQ ID NO 10
LENGTH: 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat peptide
LOCATION: (61)..(714)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: sig peptide LOCATION: (1)..(60)
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LOCATION: (1)..(714)
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Best Local Similarity
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US-10-384-933-10
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OTHER INFORMATION: hen egg-white lysozyme (HEL) monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Winter, Gregory
APPLICANT: Winter, Gregory
APPLICANT: Bonert, Timothy
TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
FILE REFERENCE: 213839-00013
CURRENT APPLICATION NUMBER: US/09/726,219A
PRIOR PPLICATION NUMBER: GB 9015198.6
PRIOR PLING DATE: 1990-07-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 AICACATGICGAGCAAGTGGGAATATTCAAAATTATTAGCATGGTATCAGCAGACACAG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 GGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGTGCCATCA 283
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80.5%; Pred. No. 1.8e-75;
ative 0; Mismatches 127; Indels 0;
                                                                                        APPLICANT: Cambridge Antibody Technology
APPLICANT: Cambridge Antibody Technology Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1991-03-06
PRIOR APPLICATION NUMBER: GB 9110549.4
PRIOR FILING DATE: 1991-05-15
PRIOR APPLICATION NUMBER: PCT/GB91/01134
PRIOR FILING DATE: 1991-07-10
PRIOR APPLICATION NUMBER: US 07/971,857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/484,893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: GB 9022845.3
PRIOR FILING DATE: 1990-10-19
PRIOR APPLICATION NUMBER: GB 9024503.6
PRIOR FILING DATE: 1990-11-12
PRIOR APPLICATION NUMBER: GB 9104744.9
PRIOR FILING DATE: 1991-03-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1990-10-19
APPLICATION NUMBER: GB 9022845.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9022845.3
                                                  Sequence 189, Application US/09726219A GENERAL INFORMATION:
                                                                                                                                        Medical Research Council
                                                                                                                                                                                                                            Hoogenboom, Hendricus
Griffiths, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                 Clackson, Timothy
Chiswell, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1993-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1995-06-07
                                                                                                                                                              McCafferty, John
                                                                                                                                                                                                                                                                                       Holliger, Kasper
                                                                                                                                                                                                                                                                      Jackson, Ronald
                                                                                                                                                                                                        Johnson, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                  Pope, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 272
                                                                                                                                                                                                                                                                                                               Marks, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                        JS-09-726-219A-189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IS-09-726-219A-189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 189
                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                     APPLICANT
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                                                                                                                                                                                                                                                                                                           APPLICANT
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TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED TITLE OF INVENTION: ANTIBODIES FILE REFERENCE: 1087-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 82.1%; Pred. No. 5.4e-75;
Similarity 82.1%; Pred. No. 5.4e-75;
22; Conservative 2; Mismatches 110; Indels 2;
                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/251,215
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: US 60/323,537
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/379,980
                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: US 60/323,544
               Sequence 47, Application US/10251215 GENERAL INFORMATION:
                                                                      APPLICANT: Bowdish, Katherine S.
                                                                                                APPLICANT: Kretz-Rommel, Anke APPLICANT: Frederickson, Shana
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 522; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: murine
-10-251-215-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 47
LENGTH: 702
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531 ACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTT 590

471 AGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTTCTTGAACAACTTCTACCCCAAAG 530

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SULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     592 GACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAA 651
                                                                                               75 C--AACTGCCAGCTCAAGTGTAAGWTACATGCACTGGTTCCAGCAGAAGCCAGGCACTTC 132
                                                                                                                                                                  133 ICCCAAACICIIGAIITATAGCRCAICCAACCIGGCIICIGGAGICCCIGCICGCIICAG 192
                                                                                                                                                                                                                   352 TGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGACCAA 411
                                                                172 TCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAATC 231
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112 GATGACTCAGTCTCCAGCCTCCCTATCTGCAGGAGAAACTGTCACCATCACATG 171
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Segmental	Segmence 3 Appli	Segmence 13035 A	Segmence 3 Appli		ì	- α	α			10,1		Sequence 4 Appli	. 4	٠ ٦	Sequence 4 Appli			TIAN /C SSUSSESS	Seguence 300, App	Sequence 5847, Ap
	US-09-770-916-3	JS-08-480-120-3	02-25766-13035	US-08-090-534-3	US-07-904-074A-1	JS-07-904-074A-5	8-900-89-80-sn	US-09-897-511A-8	US-09-897-006-13	US-09-897-511A-13	US-07-743-329-4	JS-08-303-569-4	JS-08-485-686-4	US-08-846-658A-4	-846-658B-4	US-09-348-224-4	US-09-795-515-4	15-08-462-767-3	US-60-168-599-386	JS-60-360-207-21147	US-09-724-671-5847
ΩI	60-SD	US-08-4	PCT-US	US-08-	US-07-	US-07-9	.60-Sn	-60-SD	-60-SN	-60-SN	US-07-7	US-08-3	US-08-4	-80-Sn	ns-08-	-60-SD	-60-SD	US-08-4	-09-SI	-09-SD	-60-SD
DB	30	8	~	4	m	٣	33	33	33	33	٣	7	80	12	12	17	30	8	09	80	29
% Query Match Length DB	979	937	966	751	1041	1041	5711	5711	6255	6255	943	943	943	943	943	943	943	882	764	2221	709
% Query Match	100.0	78.6	74.9	72.4	70.8	70.8	64.8	64.8	64.8	64.8	62.9	62.9	65.8	62.8	65.9	62.9	62.8	61.1	59.7	58.9	57.1
Score	979	769.6	733.6	708.6	693.4	693.4	634.2	634.2	634.2	634.2	615.6	615.6	615.6	615.6	615.6	615.6	615.6	598	584.8	576.6	558.8
Result No.	1	7	æ	4	2	9	7	80	0	10	11	12	. 13	14	15	16	17	18	19	20	21

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                Sequence 10262, A Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli
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Sequence 56, Appl
Sequence 56, Appl
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Sequence 192, App
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Sequence 48, Appl
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Sequence 21, Appl
Sequence 3, Appli
Sequence 3, Appli
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                                                                    Sequence 121, App
Sequence 121, App
                                                                                        Sequence 22, Appl
Sequence 4, Appli
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APPLICANT: Yahr, Timothy L.
APPLICANT: Sawa, Teiji
APPLICANT: Fritz, Robert B.
TITLE OF INVENTION: Method of and compositions for immunization with the TITLE OF INVENTION: Pseudomonas V antigen
FILE REFERENCE: 650053.91487
                                                                                                                                                                                                               Sequence
           US-09-903-327A-3
US-09-724-671-10262
                                                                                                           US-09-724-671-7170
                                                US-08-373-297-7
US-07-688-197-1
PCT-US01-18569-121
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                                                                                 US-10-264-049-121
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US-08-350-400A-56
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US-10-006-773-18
                                                                                         PCT-US01-14151-22
                                                                                                                                                                                                       US-09-454-925A-9
                             US-09-237-061-1
                                                                                                                                                    US-08-467-175-56
                                                                                                                                                                        US-08-467-564-56
                                                                                                   US-08-157-101-4
                                        US-08-070-160-7
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                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/770,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/126,794
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/448,339 PRIOR FILING DATE: 1999-11-23
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PRIOR APPLICATION NUMBER: 60/109,952
                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09770916
GENERAL INFORMATION:
APPLICANT: Frank, Dara W.
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633
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1106
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LOCATION: (44)..(103)
NAME/KEY: V_region
LOCATION: (104)..(172)
OTHER INFORMATION: FRI
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LOCATION: (251)..(271)
OTHER INFORMATION: CDR2
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LOCATION: (206)..(250)
OTHER INFORMATION: FR2
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LOCATION: (173)..(205)
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   ORGANISM: mouse
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LENGTH: 979
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781 CCCAGCTCCATCCTATCTTCCCTTCTAAGGTCTTGGAGGCTTCCCCACAAGCGACCTACC 840
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                                                                                                                                                                                            100.0%; Score 979; DB 30;
100.0%; Pred. No. 2.3e-125;
vative 0; Mismatches 0;
                                                                                                                                                                                                                                   Matches 979; Conservative
                                                                             NAME/KEY: V_region
LOCATION: (455)..(487)
OTHER INFORMATION: FR4
NAME/KEY: C_region
LOCATION: (428)..(745)
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             OTHER INFORMATION: FR3
                                            (394)
LOCATION: (272)..(367)
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                                NAME/KEY: V_region
LOCATION: (368)..(3
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TITLE OF INVENTION: Gene Expression Profiles in Glomerular Diseases
FILE REFERENCE: 44921-5068-WO
CURRENT APPLICATION NUMBER: PCT/USO2/25766
CURRENT FILING DATE: 2002-08-14 941 TGAGTCTTTGCAAAAAAAAAAAAAAAAAAAAAAAAA 976 902 TGAGTCTTTGCACTTGAAAAAAAAAAAAAAAAAAA 937 ; Sequence 13035, Application PC/TUS0225766 ; GENERAL INFORMATION: PRIOR APPLICATION NUMBER: US 60/311,837 PRIOR FILING DATE: 2001-08-14

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19406-2799
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LOCATION:
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                                                                                                                                                                                                                                                                                                       97 CAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 GGAGTATGAAGATATGGGAATTTATTATTGTCTACAGTATGATGAGTTTCCTCGGACGTT 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 CCCATCAAGGTTCAGTGGCAGTGGATCTGGGCAAGATTATTCTCTCACCATCAGCAGCAT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 GCAGCCIGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTT 396
                                                                                                                                                                                                                                                                   79 CAIGGACAIGAGGACCCCIGCICAGIIICIIGGAAICIIGIIGCICIGGIIIICCAGGIAI 138
                                                                                                                                                                                                                                                                                                                                            139 GAAAIGIGACAICAAGAIGACCCAGICICCAITCCAIGIAIGCAICICIAGGAGAGAG 198
                                                                                                                                                                                                                                                                                                                                                                                  157 TGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCA 216
                                                                                                                                                                                                                                                                                                                                                                                                         277 GCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCT 336
                                                                                                                                                                                                                                37 CACAGTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGCTGTGGCTTACAGGTGC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 GACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGT
                                                                                                                                                                                              0; Gaps
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                                                                                                                                                           Similarity 87.6%; Pred. No. 1.2e-91; Pred. No. 1.2e-91; Similarity 87.6%; Pred. No. 1.2e-91; Similarity 87.6%; Pred. Nismatches 114; Indels
                                                                                                     OTHER INFORMATION: Genbank Accession No. S65921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          937 AAAGTGAGTCTTTGCA 952
                                                                                                                                                                                                   Matches 802; Conservative
                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                       r-0S02-25766-13035
           SEQ ID NO 13035
                              LENGTH: 998
                                                                                                                                                               Query Match
                                                                                                                                                                                    Best Local
                                                                                    FEATURE:
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TITLE OF INVENTION: Recombinant and Humanized IL-1 beta TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory TITLE OF INVENTION: Disorders in Man
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 GTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTAGCA 205
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                                                                                                                                                                                                                                                                                                                                                                                                      SmithKline Beecham Corporation - Corporate Patents
                                                                                                                                                                                                                                                                                  Recombinant and Humanized IL-1 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/090,534 FILING DATE: 19930719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: SEC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5090
TELEFAX: 215-270-5090
                                                                                                                Sequence 3, Application US/08090534 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
979 AAAGTCAGTCTTTGCA 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 215-270-5090 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                               APPLICANT: Young, Peter
APPLICANT: Gross, Mitchell
APPLICANT: Jonak, Zdenka L.
APPLICANT: Theisen, Timothy
APPLICANT: Hurle, Mark
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            714; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      King of Prussia
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266 GCAGAIGGIGIGCCAICAAGGIICAGIGGCAGIGGAICAGGAACACAAIAIICICICAAG 325
             326 AICAACAGCCIGCAGCCIGAAGAITITIGGGAGITATIACIGICAACAITITIGGAGIACI 385
                                                                    CCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACT 445
                                                                                                                                                               GIATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGC 505
                                                                                                                                                                                                                    TICTIGAACAACITCIACCCCAAAGACAICAATGICAAGIGGAAGAITGAIGGCAGIGAA 565
                                                                                                                          566 CGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAGAAGACAGCACCTACAGC 625
                                                                                                                                                                             526 ATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGT 685
                                                                                                                                                                                                                                                                                                                                                                                 686 GAĠGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT 745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROY PAXTON
APPLICANT: Y.H. JOY YANG
TITLE OF INVENTION: Chimeric Anti-CEA Antibody
NUMBER OF SEQUENCES: 10
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19920615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States of America ZIP: 91010-0269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/07904074A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1500 East Duarte Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: NOT TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               John E. Shively
Rainer Fischer
Anna Wu
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202) 785-5351
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APPLICANT:
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56 ACTCAGGTCCTGGCGTGCTGCTGTGTGCGTGCCAGATGTGACATCCAGATG .115
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                                                                                                                                                                                                                                                          70.8%; Score 693.4; DB 3; Length 1041; 85.0%; Pred. No. 4e-86; tive 0; Mismatches 136; Indels 3;
                                                                                                                                                                     Synthetically Prepared
                                                                                                                                                        Prepared
                                                               Single Stranded
                                                                                                                                       Not Applicable Synthically F
                                                                                                                                                                                                            PUBLICATION INFORMATION: None
                                                                                     MOLECULE TYPE: Nucleic Acid
HYPOTHETICAL: Not Applicable
                                                                                                                    ANTI-SENSE: Not Applicable
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                IMMEDIATE SOURCE: Synthet POSITION IN GENOME: None
                                                                                                                                                                                                                                                                                        Matches 788; Conservative
                                              NUCLEIC ACID
                                                                             Unknown
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                    FRAGMENT TYPE: NORIGINAL SOURCE:
                                                           STRANDEDNESS:
                                                                                                                                                                                               FEATURE: None
                                                                         TOPOLOGY:
                                                                                                                                                                                                                ; PUBLICATION US-07-904-074A-1
                               LENGIH:
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893 ITCCTTGGCTTTTATCATGCTAATATTTGCAGAAAATATTCAATAAAGTGAGTCTTTGCA 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: 3M Double Density 5 1/4" diskette
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ROY Paxton
APPLICANT: Y.H. JOY Kang
TITLE OF INVENTION: Chimeric Anti-CEA Antibody
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                        953 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 979
                                                                                                                                                                                                              946 CTTGAAAAAAAAAAAAAAAAAAAA 972
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APPLICATION NUMBER: US/07/904,074A
FILING DATE: 19920615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RY: United States of America 91010-0269
                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/07904074A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: None TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 785-5938 TELEFAX: 440087 LM WSH INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single Stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1500 East Duarte Road
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NAME: Irons, Edward S.
REGISTRATION NUMBER: 16,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: None
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APPLICANT: Rainer Fischer
APPLICANT: Anna Wu
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                                                                                                                                                                                                                                                                                                     -07-904-074A-5
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893 TICCITGGCTITIAICATGCTAATAITTGCAGAAAATAITCAATAAAGTGAGTCTITGCA 952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 AGTTATTACTGTCAACATTTTTGGAG---TACTCCGTACACGTTCGGAGGGGGACCAAG 412
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                                                                                                                                                            226 AAAGCACTGATTTACTCGGCATCCTACCGTTACAGTGGAGTCCCTGATCGCTTCACAGGC 285
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116 ACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTCACCATCACATGTCGA 175
                  176 GCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCT 235
                                                                                  953 AAAAAAAAAAAAAAAAAAAAAAAA 979
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FILE REFERENCE: GALA-06415
CURRENT APPLICATION NUMBER: US/09/897,006
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,851
PRIOR FILING DATE: 2000-07-03
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; GENERAL INFORMATION:
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                                                                                                                             Score 634.2; DB 33; Length 5711;
Pred. No. 5e-78;
0; Mismatches 68; Indels 0;
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NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                             64.8%;
90.8%;
                                                                                     OTHER INFORMATION: Synthetic
                                                                                                                                                 Matches 675; Conservative
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                        SEQ ID NO 8
LENGTH: 5711
                                                                                                 8-900-68-60-sn
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Sequence 8, Application US/09897511A GENERAL INFORMATION: APPLICANT: Bremel, Robert APPLICANT: Miller, Linda

-09-897-511A-8

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2461 GTCTCCAGCCTCCCTATCTGCATCTGCGAGAAACTGTCACTATCACATGTCGAGCAAG 2520
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               TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors FILE REFERENCE: GALA-06416
                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                          CURRENT APPLICATION NUMBER: US/09/897,511A CURRENT FILING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: 60/215,925 PRIOR FILING DATE: 2000-07-03
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Bleck, Gregory
                                                                                                                                                  NUMBER OF SEQ ID NOS: 36
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  APPLICANT:
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Best Local S
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LENGTH: 6255
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                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/897,006
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,851
                                                                                               TITLE OF INVENTION: Expression Vectors FILE REFERENCE: GALA-06415
                                  Sequence 13, Application US/09897006 GENERAL INFORMATION:
                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                         PRIOR FILING DATE: 2000-07-03
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Matches 675; Conservative
                                                                                APPLICANT: Bleck, Gregory
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4070 GGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCACACTAGACCAAGGACGAGTA 4129
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APPLICANT: Bleck, Gregory
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
FILE REFERENCE: GALA-06416
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/897,511A CURRENT FILING DATE: 2001-06-29
                                                   4250 CCTCCCCCCCCTAACGTTACT 4272
781 CCCAGCTCCATCCTATCTTCCCT 803
                                                                                                                                                                            Sequence 13, Application US/09897511A GENERAL INFORMATION:
APPLICANT: Bremel, Robert
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,925
PRIOR FILING DATE: 2000-07-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Synthetic US-09-897-511A-13
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276 TGCCATCAAGGTTCAGTGGAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCC 335
                                                                                         336 IGCAGCCTGAAGATTTTGGGAGTTA†TACTGTCAACATTTTTGGAGTACTCCGTACACGT 395
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                                                                                                                                                                                                                                          456 TCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACA 515
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STREET: One Liberty Place - 46th | Floor
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08303569 GENERAL INFORMATION:
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APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
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                   4190 CAAGAGCTTCAACAGGAATGAGTGTTGAAAGCATCGATTTCCCCTGAATTCGCCCCTCTC 4249
661 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGT 720
                                                                        721 CAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAGCTC 780
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                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Humanised Antibodies NUMBER OF SEQUENCES: 28
                                                                                                                                                                                    4250 CCTCCCCCCCCTAACGTTACT 4272
                                                                                                                                                781 CCCAGCTCCATCCTATCTTCCCT 803
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                                                                                                                                                                                                                                                                              Sequence 4, Application US/07743329 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
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REGISTRATION NUMBER: 33,712
REFERENCE/DOCKET NUMBER: CA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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FILING DATE: 19910917
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84..722
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Best Local 9
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636 CCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTC 695
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                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: CARP-0009 TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 base pairs
                                                                                               APPLICATION NUMBER: US 07/743,329 FILING DATE: 17-SEP-1991 ATTORNEY/AGENT INFORMATION:
                   APPLICATION NUMBER: US/08/303,569
                                                                                                                                                                   NAME: Hohenschutz, Liza D. REGISTRATION NUMBER: 33,712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat_peptide LOCATION: 84..722
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                           FILING DATE
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816 GAGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCCCACCTCC 875
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696 ACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAA 755
                756 GGTCCTGAGACGCCACCACCAGCTCCCAGCTCCTATCTTCCCTTCTAAGGTCTTG 815
                                                                                      62.9%; Score 615.6; DB 8; Length 943; 84.6%; Pred. No. 2e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
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APPLICATION NUMBER: US/08/485,686
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                            936 TAAAGTGAGTCTTTGCAAAAAAAAAAAAAAAA 969
                                                                                                                                                                                                                                                                                                                910 TAAAAGTGAGTCTTTGCCTTGAAAAAAAAAAA 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hohenschutz, Liza D.
REGISTRATION NUMBER: 33,712
REFERRENCE/DOCKET NUMBER: CARP-0009
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APPLICATION NUMBER: US 07/743,329
FILING DATE: 17-SEP-1991
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELERAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
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nucleic acid
EDNESS: single
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84..722
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                                                                                                                     156 CTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTAGCATGGTATCAGC 215
                                                                           76 CCAGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGA 135
                                                                                                                                                     136 AGGTCACCATGACCTGCAGTCCCAGCTCAAGTGT---AAGTTACATGAACTGGTACCAGC 192
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739; Conservative
Matches
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APPLICANT: Athwal, Diljeet S.
APPLICANT: Enteage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

Sequence 4, Application US/08846658A GENERAL INFORMATION:

S-08-846-658A-4

APPLICANT: Adair, John R.

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96 CCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 CCAGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGA 135
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ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0 Version #1.25
CURRENT APPLICATION DATA:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
RESISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARE
                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                               Floppy disk
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nucleic acid
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LOCATION: 84..722
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Best Local Similarity
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LOCATION: 84..722
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                                                             636 CCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTC 695
                                                                                                                          696 ACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAA 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Woodcock Washburn Kurtz Mackiewicz & Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                        936 TAAAGTGAGTCTTTGCAAAAAAAAAAAAAAAA 969
                                                                                                                                                                                                                                                                                                                                                                                                      910 TAAAGTGAGTCTTTGCCTTGAAAAAAAAAAAA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Adalr, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFLING DATE: 01-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08846658B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Trujlllo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARE
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TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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GAGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCCCACCTCC 875
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                                                                                                                         96 CCAGATGIGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCCATCTGTGGGAGAAA 155
                                                                                                                                                      156 CTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGC 215
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                                                                                   6; Gaps
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                                                                                   0; Mismatches 129; Indels
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US-08-846-658B-4
                                          Query Match
                                                                                            Matches
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CCC7 20.11.01

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2003, 22:24:31 ; Search time 159.035 Seconds
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9033.299 Million cell updates/sec

ritle:
US-09-770-916-3
Perfect score: 979
Sequence: 1 acaccettgetggagtcag......aaaaaaaaaaaaaaaaaa 979

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Appl

Published_Applications_NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•	Description	Sequipos 8 and 1	Sequence 8 Appli	Segmence 13 Appl	Secuence 13 Appl	Segment A shall	Sequence 4, Appril	Sequence 3, Appril	Sociondo 20 anal	Sociones 29, Appl	Sednence 18, Appl	sednence IO, Appl	Sequence 17, Appl	Sequence 10. Appl	Sequence 79 April	Segmence 11 Appl	Sequence 11 April	compact 11, Appr	Jednemce 81, Appl	Sequence 18, Appl	Segmence 125 App	Sequence 68. April	-13: (a. a	
SUMMARIES	ID	US-09-897-511A-8	0.00-897-006-8	US-09-897-511A-13	US-09-897-006-13	US-09-795-515-4	US-09-903-327A-3	US-09-237-061-1			TC-10-216-404-10	07 - 404 - 70 CO	US-10-1/6-380-1/	COS-10-006-773-10	US-09-800-729-79	US-09-897-511A-11			TC-10-1E3-303-10	_	US-10-216-484-125	US-10-158-646-68		
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40.7	39.9	39.8	39.6	39.6	39.6	39.4	39.4	39.3	39.2	38.4	38.1	38.1	37.8	37.8	37.8	37.8	37.6	37.6	37.6	37.4	37.3	37.3	37.2	36.6	36.5	
398.4	390.6	389.8	387.4	387.4	387.4	385.8	385.8	384.4	384.2	376.4	373	373	369.8	369.8	369.8	369.6	368.2	368.2	368.2	366.4	365.6	365.2	364.6	358.6	357	
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ALIGNMENTS

pplication b. US20030 MATION: emel, Robolilleck, Lilick, Lilick, Lilick, Care NATION: Hog CATION NUM C DATE: C DATE: C DATE: C DATE: C DATE: C TION NUMBI C DATE: C TION STATE Entin Vers	Query Match 64.8%; Score 634.2; DB 9; Length 5711; Best Local Similarity 90.8%; Pred. No. 1.3e-156; 1.3e-156; Matches 675; Conservative 0; Mismatches 68; Indels 0; Gaps 0; 0; Gaps 120 1 GGTCCTGGCGTGCTGTGGCTTACAGGTGCCAGATGCAGATGCAGATGACCA 120 111 1 1 1 1 1 1 1 1 1
RESULT 1 US-09-897-511A-8 Sequence 8, Ap. Publication No. GEMERAL INFORM APPLICANT: BT. APPLICANT: BT. TITLE OF INVE. TITLE OF INVE. CURRENT APPLICANTINE OF REAL OF SEQ. CURRENT APPLICANTINE OF SEQ. CURRENT APPLICANTINES. NUMBER OF SEQ. SOFTWARE: PALCANTINES. SOFTWARE: PALCANTINES. LENGTH: 5711 TYPE: DNA ORGANIES. FEATURE: CORGANIES. FEATURE: CORGANIES.	Query Match Best Local Matches 67 Oy 61 Oy 121 Oy 121 Oy 181 Ob 2521 Oy 241
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APPLICANT: Miller, Linda
APPLICANT: Miller, Linda
APPLICANT: Miller, Linda
APPLICANT: Miller, Gragory
TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors
FILE REFERENCE: GALA-06416
CURRENT APPLICATION NUMBER: US/09/897,511A
CORRENT FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-07-03
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90.8%; Pred. No. 1.4e-156;
tive 0; Mismatches 68;
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NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
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               2581 CCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGG 2640
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TITLE OF INVENTION: Expression Vectors
TITLE REFERENCE: GALA-06415
CURRENT APPLICATION NUMBER: US/09/897,006
CURRENT FILING DATE: 2001-06-29
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Patent No. US20020106729A1
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GENERAL INFORMATION:

8-900-86-60-9

Query Match

SEO ID NO 8

NUMBER OF

SOFTWARE:

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-09-897-006-8

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US-09-897-006-13

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ESULT 4

S-09-897-006-13

Sequence 13, Application US/09897006

Patent No. US20020106729A1

GENERAL INFORMATION:

APPLICANT: Bleck, Gregory

TITLE OF INVENTION: Expression Vectors

FILE REFERENCE: GLA-06415

FILE REFERENCE: GLA-06415

PRIOR FILING DATE: 2001-06-29

PRIOR PLILING DATE: 2001-06-29

PRIOR FLILING DATE: 2000-07-03

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin Version 3.0

SEQ ID NO 13

LENGTH: 6255
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ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Synthetic

DNA

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                                                                                                                                                                                                                     CCTGGTCTATTCTGCAAAAACCTTAqCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGG
                                ;
    DB 10; Length 6255;
                              Indels
                                68;
    Score 634.2; DB 10
Pred. No. 1.4e-156;
0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4250 CCTCCCCCCCCCTAACGTTACT 4272
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64.8%;
90.8%;
                          Matches 675; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Philadelphia
             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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CURRENT FILING DATE: 2001-07-10 PRIOR APPLICATION NUMBER: 09/613,017 PRIOR FILING DATE: 2000-07-10
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DELIVERY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 AGGICACCATGACCTGCAGTGCCAGCTCAAGTG---AAGTTACATGAACTGGTACCAGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 AGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AGAAGTCAGGCACCTCCCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Gaps
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                                                                                                                                                                                                                                                                                                                                          CARP-0057
                                                                                                                                                                    APPLICATION NUMBER: US/09/795,515
                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yarko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: CA. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             943 base pairs
                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: mat_peptide LOCATION: 84..722
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                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                         FILING DATE
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                   COUNTRY:
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STATE:
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APPLICANT: Li, Erguang
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TAR
TITLE OF INVENTION: GENE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 GTCACCATCACATGTCGAGCAAGTGGGAATATTCAA-------AATTATTAGCA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GCCACCATCTCCTGCAAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTATATGAAC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 AGAIGIGACAICCAGAIGACICAGICICCAGCCICCCIAICIGCAICIGIGGGAGAAACI 157
                                                                                                                                                                                                                                                                                                                                                                      756 GGTCCTGAGACGCCACCACCAGCTCCCAGCTCCTATCTTCCCTTCTAAGGTCTTG 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 876 TICICCICCICCITICCITICCITIGGCITITATCAIGCIAAIATTIGCAGAAATATICAA 935
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                                                                                                                  38 ACAGICAIGAGIGIGCICACICAGGICCIGGCGIIGCIGCIGCIGIGGCIIACAGGIGCC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.6%; Score 535; DB 9; Length 831;
80.4%; Pred. No. 7.2e-131;
tive 0; Mismatches 145; Indels 12; Gaps
                                                                                             636 CCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTC
                                                                                                                                                                                        696 ACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAA
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; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 936 TAAAGTGAGTCTTTGCAAAAAAAAAAAAAAAA 969
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FILE REFERENCE: 22908-1228
CURRENT APPLICATION UMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
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PRIOR FILING DATE:
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GCAGATGGTGTGTCAAGGTTCAGTGGCAGTGGATCAGGAACACAAATATTCTCTCAAG 325
                                                                         326 ATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACT 385
                                                                                                                                                       307 Arccarccreregageageageargcrecrerarrarracreregeaaacraargagear 366
                                                                                                                                                                                         386 CCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACT 445
                                                                                                                                                                                                                GTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGC 505
                                                                                                                                                                                                                                                                                 ATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGT 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  746 TAGAGACAAAGGTCCTGAGACGCCACCAGCTCCCCAGCTCCATCCTATCTTCCCTTC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin TITLE OF INVENTION: Antagonist/Agonist Mediated Disease States FILE REPERENCE: DM-6956 ... 0X/09/237,061 CURRENT APPLICATION NUMBER: US/09/237,061 PRIOR APPLICATION NUMBER: 60/072,733 PRIOR PRIING DATE: 1998-01-27
                                                                                                                                                                                                                                                                                                                                  506 ITCTIGAACAACTICTACCCCAAAGACATCAATGTCAAGIGGAAGAITGATGGCAGIGAA
                                                                                                                                                                                                                                                                                                                                                                                                          CGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAAGACAGCACCTACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09237061
Patent No. US20020081624A1
GENERAL INFORMATION:
APPLICANT: DuPont Pharmaceuticals Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              806 TAAGGICTIGGAGGCTICCCC 826
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Best Local Similarity
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44 ATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGT 103

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GGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGTGCCATCA 283
                                                                         104 GACATCCAGATGACTCAGTCTCCAGGCTCCCTATCTGCATCTGTGGGAGAAACTGTCACC 163
                                                                                                                                                                                164 ATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAG 223
                                                                                                                                                                                                              284 AGGITCAGIGGCAGIGGATCAGGAACAATAITCICTCAAGAICAACAGCCIGCAGCCT 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             524 CCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTG 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 GGGACCAAGCTGGAAATAAAACGGGCpGATGCTGCACCAACTGTATCCATCTTCCCACCA 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 TTGACCAAGGACGAGTATGAACGACAȚAACAGCTATACCTGTGAGGCCACTCACAAGACA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            611 CTGAGCAAAGCAGACTACGAGAAACA¢AAAGTCTACGCCTGCGAAGTCACCCCATCAGGGC 670
GENERAL INFORMATION:
APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, No. US2020102658Alyaki
APPLICANT: Hori, No. US2020102658Alyaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL UŞE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                671 CTGAGCTCGCCCGTCACAAGAGCTTÇAACAGGGGAGAGTGTTA 714
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/09859053 Patent No. US20020102658A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-05-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    697 CAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                337 GCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTT 396
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70.1%; Pred. No. 2.6e-109;
tive 0; Mismatches 268; Indels 11; Gaps
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655; Conservative
                                                                  LOCATION: (39)...(746)
NAME/KEY: 3'UTR
LOCATION: (750)...(974)
NAME/KEY: S19_Peptide
LOCATION: (39)...(104)
-09-859-053-29
                        (1)...(38)
CDS
5'UTR
  NAME/KEY:
                        LOCATION:
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                                                 NAME/KEY:
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APPLICANT: Junghans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor
FILE REFERENCE: 003
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46.3%; Score 453; DB 12; Length 698;
Best Local Similarity 79.8%; Pred. No. 2.5e-109;
Matches 534; Conservative 0; Mismatches 135; Indels
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936 TAAAGTGAGTCTTTGCAAAAAAAAAAAAAAAA 969
                     CURRENT APPLICATION NUMBER: US/10/006,773 CURRENT FILING DATE: 2001-12-10 PRIOR APPLICATION NUMBER: 60/250,089 PRIOR FILING DATE: 2000-11-30
                                                                                                                                                  Sequence 18, Application US/10006773 Patent No. US20020132983A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                                  US-10-006-773-18
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 18
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656 GAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCC 715
                      1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.6%; Score 446.6; DB 9; Length 714;
79.0%; Pred. No. 1.2e-107;
tive 0; Mismatches 134; Indels 12; Gaps
                                                                                                                                                                                                                                                                             APPLICANT: Serizawa, No. US20030103976Alufusa
                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                               APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                Sequence 10, Application US/10216484
Publication No. US20030103976A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549; Conservative
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SEQ ID NO 10
LENGTH: 714
                                                                                                                     690 ATCGTCAAG 698
                                                                              716 ATTGTCAAG 724
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; LOCATION: (1)..(60)
US-10-216-484-10
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APPLICANT: van Rooijen, Gijs APPLICANT: woloney, Maurice TITLE OF INVENTION: Methods for the TITLE OF INVENTION: Compositions FILE REFERENCE: 9369-226 • OTHER INFORMATION: The Linin promoter-secretion signal D9 light chain - linin ter OTHER INFORMATION: ator cassette 531 ACATCAATGTCAAGTGGAAGATTGÅTGGCAGTGAACGACAAAATGGCGTCCTGAACAGTT 590 380 AGCIGGAAAICAAACGGGCIGAIG¢IGCACCAACIGIAICCAICIICCCACCAICCAGIG 439 471 AGCAGTTAACATCTGGAGGTGCCT¢AGTCGTGTGCTTCTTGAACAACTTCTACCCCCAAAG 530 591 GGACTGATCAGGACAGCAAAGACACCTACAGCATGAGCAGCACCTCACGTTGACCA 650 651 AGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 710 90 CAGGIGCCAGAIGIGACATCCAGAIGACICCAGICTCCCAGCCICCCIAICIGCAICIGIGG 149 252 CIGCAAAAACCITAGCAGAIGGIGIGIGCATCAAGGIICAGIGGCAGIGGAICAGGAACAC 311 ------TCGAGCAAGTGGGAATATTC 191 192 AAAATTATTTAGCATGGTATCAGCAĠACACAGGGAAAATCTCCTCCAGCTCCTGGTCTATT 251 45.5%; Score 445.4; DB 9; Length 3344; 80.2%; Pred. No. 5e-107; Live 0; Mismatches 116; Indels 18; Gaps 711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT 745 680 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGT 714 CURRENT APPLICATION NUMBER: US/10/176,380 CURRENT FILING DATE: 2002-06-21 PRIOR APPLICATION NUMBER: US 10/032, 201 Sequence 17, Application US/10176380 Publication No. US20030093832A1 GENERAL INFORMATION: 150 GAGAAACTGTCACCATCACATG---2002-06-21 PRIOR FILING DATE: 2001-12-19 NUMBER OF SEQ ID NOS: 37 SOFTWARE: PatentIn version 3.1 ORGANISM: Artificial Sequence Matches 543; Conservative APPLICANT: Szarka, Steven ; LOCATION: (2054)..(2790) ; OTHER INFORMATION: US-10-176-380-17 Best Local Similarity NAME/KEY: exon US-10-176-380-17 3344 SEQ ID NO 17 TYPE: DNA Query Match FEATURE: LENGTH:

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684 GTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGT 743
                                                                                                                                                                                                                                    504 GCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTG 563
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                                                                                                                                                                               444 CIGTATCCATCTTCCCACCATCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGT 503
                                                                                                                                                                                                                                                                                                                                       264 TAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCA 323
                                                                                                 324 AGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTA 383
204 CATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAACCT 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: 32 Human secreted proteins FILE REFERENCE: P2044P1 CURRENT APPLICATION NUMBER: US/09/800,729 CURRENT APPLICATION NUMBER: 2001-03-08 PRIOR APPLICATION NUMBER: PCT/US00/26013 PRIOR FILING DATE: 2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n equals a,t,g, or c US-09-800-729-79
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; Patent No. US20020068319A1
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PRIOR FILING DATE: 1999-0
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TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2355 ATTICACICITACCATCAGCAGTGGCAGGCTGAAGACCTGGCAGATTACTTCTGTCAGC 2414
                                                                                                                             2415 AACATTATAACACTCCTCCCACGTTCGGTGCTGGGACCAGGTGGAGCTGAAACGGGCTG 2474
                                                                                                                                                                                         2475 AIGCIGCACCAACTGIAICATCTCCCACCAICCAGTGAGCAGTAACAICIGGAGGIG 2534
                                                                                                                                                                                                                                                                        2533 CCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGA 2594
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                                                                                                                                                                                                                                                                                                                                 552 TTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAG 611
                                                                                                                                                                     432 ATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTG 491
                                                                                                                                                                                                                                                      492 CCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGA 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.4%; Score 444.6; DB 12; Length 729; Best Local Similarity 77.3%; Pred. No. 4.2e-107; Matches 559; Conservative 0; Mismatches 149; Indels 15; Gaps
                                                                                          372 ATTITIGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (15)..(410)
OTHER INFORMATION: 3D8 Light chain V region, plus leader
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/10006773 Patent No. US20020132983A1 GENERAL INFORMATION:
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SEQ ID NO 10
LENGTH: 729
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. 41 GTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGTGGGTGCCTTACAGGTGCCAGA 100 Gaps

FILE REFERENCE: GALA-06416
CURRENT APPLICATION NUMBER: US/09/897,511A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,925
PRIOR FILING DATE: 2000-07-03

PatentIn version 3.0

NUMBER OF SEQ ID NOS: 36

; ORGANISM: Artificial Sequence ; FEATURE: ; OTHER INFORMATION: Synthetic US-09-897-511A-11

5691

SEQ ID NO 11 LENGTH: 56 TYPE: DNA

SOFTWARE:

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TGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAACTGTC 160
                                                                                                                        161 ACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACA 220
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                                                                                     65 receacarccascreactrectrectrectrectrectrectreserrectresecarcer 124
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701 ACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCC 760
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9917 GGCACCTCCCCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAGTCCCTGCT 3976
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                                                                                                                      164 ATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAG 223
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Similarity 80.2%; Pred. No. 7e-103; Pred. No. 7e-103; Indels 0; Mismatches 125; Indels
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; Patent No. US20020106729A1
; GENERAL INFORMATION:
                             531; Conservative
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APPLICANT: Miller, Linda APPLICANT: Bleck, Gregory TITLE OF INVENTION: Host Cells Containing Multiple Integrating Vectors

Sequence 11, Application US/09897511A Publication No. US20030092882A1 GENERAL INFORMATION:

-09-897-511A-11

SCULT 14

APPLICANT: Bremel, Robert

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3860 ATGACCTGCAGTGCCACCTCAAGTGT -- - AAGTTACATACACTGGTACCAGCAGAAGTCA 3916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 ATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAG 223
                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 5691;
                                                                                                                                                                                                                                                                                                                                                            Query Match

43.9%; Score 430; DB 10; Length 56
Best Local Similarity 80.2%; Pred. No. 7e-103;
Matches 531; Conservative 0; Mismatches 125; Indels
APPLICANT: Bleck, Gregory
TITLE OF INVENTION: EXPRESSION Vectors
FILE REFERENCE: GALA-06415
GURRENT APPLICATION NUMBER: US/09/897,006
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 60/215,851
PRIOR APPLICATION NUMBER: 60/215,851
PRIOR FILING DATE: 2000-07-03
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          earch completed: June 24, 2003, 02:04:58 ob time : 164.035 secs
                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic -09-897-006-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4454 CA 4455
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LENGTH: 5691
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OM nucleic - nucleic search, using sw model

Run on:

June 23, 2003, 20:18:11; Search time 51.8675 Seconds (without alignments) 5788:524 Million cell updates/sec

US-09-770-916-3 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

882724 Total number of hits satisfying chosen parameters: 441362 seqs, 153338381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	;	o, Appi	T,	77		7	equence 1,	æ	4	4	ς,	Sequence 2, Appli	2		TATAL / CONTRACT	٠ پ		4 ('n	26,		57,	Seguence 22, Appl		~	֡֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֓֓֓֓֓֓֓	, 000	243,	3, AE	Sequence 60, Appl
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NAME/KEY: CDS

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118-00-		-80-50	US-08-	IIS-08-		- 80 - 80	ns-08-	11S-08-	00-01	- 20 - 60	ns-08-	-60-511	000	-60-50	-60-SD	5210006-10	26135	-80-50	US-08-	115-08-		-80-S0	119-08-634-		
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	and Humanized Il-1 beta for Treatment of Il-1 Mediated Inflammatory Aan (Corporation - Corp.	Version #1.25	· ·	
-3 Application ORMATION: Young, P. Gross, M.: Jonak, Z. Theisen, I. Hurle, M.	T: Jackson, Jeffrey R. INVENTION: Recombinant INVENTION: Antibodies f INVENTION: Disorders in F SEQUENCES: 21 NUBNCE ADDRESS: SEE: SmithKline Beecham SEE: Intellectual Proper Intellectual Robert Ring of Prussia	STATE: PA COUNTRY: USA ID: 19406-2799 COMPUTER READABLE FORM: MEDIUM TYPER: FLOPPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATONIN Release #1.0, v CURRENT APPLICATION NUMBER: PT-T/1594/07560	7 7 F B B 8 C 5 C 5	LENGTH: 751 base pairs TYPE: nucleic acid STRANDEDMESS: double TOPOLOGY: unknown MOLECULE TYPE: DNA (genomic) FRAUNEE:

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Floppy disk
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 789; Conservative
                                                                                                                                                                    19910422
                                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACID
EDNESS: double
                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                       435
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              New Jersey
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Princeton
                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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                                                                                                                                                                       FILING DATE:
                                                                             MEDIUM TYPE:
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US-07-690-192-1
                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                             SOFTWARE:
                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   326 ATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACT 385
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                                                                                                               26 CACTGATCACACACAGTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGCTGTGG 85
                                                                                                                               Juery Match 72.4%; Score 708.6; DB 5; Length 751; Best Local Similarity 98.8%; Pred. No. 1.7e-161; Aatches 714; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Montano, Ximena
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: METHOD FOR INACTIVATION OF PROTEIN
TITLE OF INVENTION: FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07690192 Patent No. 5919650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS-07-690-192-1
                              r-us94-07659-3
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ADDRESSEE: Bristol-Myers Squibb Company STREET: P.O. Box 4000

NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS:

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524 CCCAAAGAÇATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTG 583
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                                Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,192
                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: DC. TELECOMMUNICATION:
COMPUTER: 'IBM PC compatible
                                                                                                                                                                                                                                             TELEPAONE: (609) 921-4163
TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 1:
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NAME: Bogden, James M
REGISTRATION NUMBER: 32,9
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261 CCTTAGCAGATGGTGTGCCATCAAĠGTTCAGTGGCAGTGGATCAGGAACACAATATTCTC 320
201 TAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAA 260
                              185 TGGCTTGGTACCAGCAGAGCCAGTCTCCTAAACTGCTGATCTATTGGGCATCCA 244
                                                                                                                              321 TCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGA 380
                                                                                       245 TAGGACATCTGGGGTCCCTGATCĢCTTCACAGGCAGTGGATCTGGGACAGATTTCACTC 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: MD
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TY: U.S. 21010-5423

COUNTRY:

FILING DATE:

SOFTWARE:

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651 AGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 710
591 GGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCA 650
                                                                                                                                                                                                       471 AGCAGTTAACATCTGGAGGTGCCTCAGTGTGTGCTTCTTGAACAACTTCTACCCCAAAG 530
                                                                            531 ACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTT 590
                                                                                                                                                                                                                                                                                                                   711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: U.S. Army Chemical and Biological Defense ADDRESSEE: Command
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Office of the Chief Counsel, Bldg E4435
Aberdeen Proving Ground
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES J.
APPLICANT: MOHYEE, ELDEFRAWI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
WUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAM 431-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08792824 Patent No. 5932449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: DAN TELECOMMUNICATION INFORMATION: TELEPHONE: 410-671-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMANUEL, PETER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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STRANDEDNESS: double
TOPOLOGY: not relevant
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21010-5423
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281 CTCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA 340
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Chain"
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                                                                                                    PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                   DAM 431-96
                                                                                                                                       APPLICATION NUMBER: US/08/792,824
                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     REGISTRATION NUMBER: 39,908
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1534
                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                LENGTH: 1644 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                            CURRENT APPLICATION DATA:
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                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                       CLASSIFICATION: 435
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OTHER INFORMATION:
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HYPOTHETICAL:

ANTI-SENSE: ORGANISM:

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STRANDEDNESS:

BALB/c pHist22

ORIGINAL SOURCE:

IMMEDIATE SOURCE

NAME/KEY: LOCATION: NAME/KEY:

LOCATION

S-08-792-824-11

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pHist 5 IMMEDIATE SOURCE:

CLONE:

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APPLICANT: MOHYEE, ELDEFRAWI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
                EMANUEL, PETER A.
                          BURANS, JAMES P.
                                        VALDES, JAMES
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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HYPOTHETICAL: N
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                                                                                                                                                                                       63.9%; Score 626; DB 2; Length 1672; 92.9%; Pred. No. 1.5e-141; tive 0; Mismatches 50; Indels
                                            /product= "antibody fragment, light
                                                                                                                    OTHER INFORMATION: /product= "antibody fragment, heavy OTHER INFORMATION: chain" /label= BotFab 5
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                                        OTHER INFORMATION:
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                 NAME/KEY: CDS
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Sequence 1, Application US/08792824 Patent No. 5932449

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Best Local Similarity 92.9%; Pred. No. 2.1e-141;
Matches 656; Conservative 0; Mismatches 50; Indels
                              ADDRESSEE: U.S. Army Chemical and Biological Defense
                                                           STREET: Office of the Chief Counsel, Bldg E4435
CITY: Aberdeen Proving Ground
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                   REFERENCE DOCKET NUMBER: DAM 431-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/792,824
                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 39,908
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4435 base pairs
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               CORRESPONDENCE ADDRESS:
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NUMBER OF SEQUENCES:
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MOLECULE TYPE: DN
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LOCATION:
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                          CLONE:
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                                                 2684 AGCAGTTAACATCTGGAGGTGCCTCAGTCGTGCTTCTTGAACAACTTCTACCCCAAAG 2743
                                                                                                                                                                           2564 TIGGGAGTIATTACTGTCAACATTTTTGGAGTACTCCGTGGACGTTCGGTGGAGGCACCA 2623
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                                411 AGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCAGTG 470
                                                                                              471 AGCAGTTAACATCTGGAGGTGCCTCAGTGGTGCTTCTTGAACAACTTCTACCCCAAAG 530
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                                                                                                                2924 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTAATAGCAAGG 2969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES J.
APPLICANT: MOHYEE, ELDEFRAMI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
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Sequence 8, Application US/08792824
Patent No. 5932449
GBNERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 39,908
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TELEPHONE: 410-671-1158
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NAME: Biffoni, U. J.
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MEDIUM TYPE: Floppy disk
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LENGTH: 1632 base pairs
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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651 AGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 GGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 AGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 GTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 TIGGGAGITALTACTGICAACAITTITGGAGIACICCGIACACGIICGGAGGGGGGGCACCA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             231 CTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA 290
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                                                                                                                                                                                                                                                                                                                           111 AGATGACTCAGTCTCCAGCTCCCTATCTGCATCTGTGGGAAAACTGTCACCATCACAT 170
                                                                                                                                                                                                                                                                                                                                                                                 171 GTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAAT 230
                                                                                                                                                                                                                                                                                                                                                                                               51 TGCTCACTCAGGTCCTGGCGTTGCTGCTGTGGGCTTACAGGTGCCAGATGTGACATCC 110
                                                                                                                                                                                                                                                                                                101 TGCCTACGGCGGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCGACATCC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 AGATGACCCAGTCTCCAGCCTCCCTATCTGCAGCTGGGAGAACTGTCACTATCACAT
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                  63.6%; Score 622.8; DB 2; Length 1632; 92.6%; Pred. No. 9e-141; Live 0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "antibody fragment, Heavy Chain"
                                                                    /product= "antibody fragment, light
                                                                                                /label= BotFab 20
                                                                                                                                                                                  /label= BotFab 20
                                                                                                                                                                                                                                                         654; Conservative
                                                                                                                                               818..1582
                                                                                                                                                            OTHER INFORMATION:
OTHER INFORMATION:
                                                                                         OTHER INFORMATION:
OTHER INFORMATION:
                                                                LOCATION: 88.798
OTHER INFORMATION:
                                                                                                                                                                                                                                           Similarity
                         pHist 20
STRAIN: BALB/C
            IMMEDIATE SOURCE:
                                                   NAME/KEY: CDS
                                                                                                                                     CDS
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07-110-910-3.rnl

5859205

Patent No.

COUNTRY:

STATE:

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456 TCCCACCATCCAGTGAGCAGTTAA¢ATCTGGAGGTGCCTCAGTCGTGCTGCTTCTTGAACA 515
                            516 ACTICTACCCCAAAGACATCAATG‡CAAGTGGAAGATTGATGGCAGTGAACGACAAAATG 575
                                                                                          576 GCGTCCTGAACAGTTGGACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCA 635
                                                                                                                                                    636 CCCTCACGTTGACCAAGGACGAGTÅTGAACGACATAACAGCTATACCTGTGAGGCCACTC 695
                                                                                                                                                                                                                                                                           696 acaacacatcaacticacccattgicaagacticaacagaatgagtiagagacaaa 755
                                                                                                                                                                                                                                                                                                                       756 GGTCCTGAGACGCCACCACCAGCTCCATCCTATCTTCCCTTCTAAGGTCTTG 815
                                                                                                                                                                                                                                                                                                                                          816 GAGGCITCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCCCACCTCC 875
                                                                                                                                                                                                                                                                                                                                                                                                     876 ITCTCCTCCTCCCTTTCCTTGG¢TTTTATCATGCTAATATTTGCAGAAATATTCAA 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock Wasburn Kurtz Macklewicz & No. 5929212ris STREET: One Liberty Place - 46 \, \text{th} \mid \text{Floor}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910 TAAAGTGAGTCTTTGCCTTGAAAAAAAAAAAAA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/743,377
FILING DATE: 10-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/116,247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 4, Application US/08116247; Patent No. 5929212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (215) 568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Paintin, Francis A. REGISTRATION NUMBER: 19,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 CIGICACCAICACAIGICGAGCAAGIGGGAATAITCAAAAITAITAGCAIGGTAICAGC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 AGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTG 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 TGCCATCAAGGTTCAGTGGCAGTGGGATCAGGAACACAATATTCTCTCAAGATCAACAGCC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 TGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTÝTTGGAGTACTCCGTACACGT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 TCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                           ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 943;
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                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                     Humanised Antibodies
                                                                                                                         STREET: One Liberty Place - 46th Floor CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                      JMBER: US/08/303,569B
07-SEP-1994
               APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Emtage, John S.
                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 943 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
LOCATION: 84..722
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                                                            TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
GENERAL INFORMATION:
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                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                                                                                                                                    MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                 FILING DATE:
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OPOLOGY:

LOCATION:

S-08-303-569B-4

Query Match

rue Jul 1 18:41:00 2003

TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 4

LENGTH: 943 base pairs TYPE: nucleic acid SEQUENCE CHARACTERISTICS:

single

TOPOLOGY: linear STRANDEDNESS:

CDS 18..722

NAME/KEY: LOCATION: 936 тадастсаттссаалалалалалалал

51 IGCTCACTCAGGICCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCC 110

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850 Trefectectecetecerrecerreserratearseratarrates 909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                733 GGTCCTGAGACGCCACCACCA-CCCAGCTCCATCTATCTTCCCTTCTAAGGTCTTG 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 ACTICTACCCCAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATG 575
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                                                                                                                                                                                                                                                                                                                                                                                               216 AGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTG 275
                                                                                                                                                                                                                                                                  193 AGAAGTCAGGCACCCCCCAAAAGATGGATTTATGACACATCCAAACTGGCTTCTGGAG 252
                                                                                                                                                                                                                                                                                                      276 TGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCC 335
                                                                                                                                                                                                                                                                                                                                       253 recerectentreaggacaeregagaceretracterecaareaggaca 312
                                                                                                                                                                                                                                                                                                                                                                         336 IGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGT 395
                                                                                                                                                            156 CTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTAGCATGGTATCAGC 215
                                                                                                                                                                                           136 AGGICACCATGACCTGCAGTGCCAGGTCT---AAGTTACATGAACTGGTACCAGC 192
                                                                                       96 CCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAA 155
                                                                                                           6; Gaps
                    Length 943;
                    62.9%; Score 615.6; DB 2; Length 984.6%; Pred. No. 4.1e-139; tive 0; Mismatches 129; Indels
                                                                   Matches 739; Conservative
                                    Query Match
Best Local Similarity
-08-116-247-4
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n
Similarity 92.2%; Pred. No. 1.3e-134;
51; Conservative 0; Mismatches 53; Indels 2;
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                                                                                                                                                                                                                                              U.S. Army Chemical and Biological Defense
                                                                                                                                                                                                                                                                               office of the Chief Counsel, Bldg E4435
Aberdeen Proving Ground
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                     DETECTION OF BOTULINUM TOXIN
 /label= BotFab 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= BotFab 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/792,824
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           Sequence 5, Application US/08792824 Patent No. 5932449
                                                                                                                                                                                       ELDEFRAWI E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Biffoni, U. J. REGISTRATION NUMBER: 39,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                         APPLICANT: EMANUEL, PETER A. APPLICANT: BURANS, JAMES P. APPLICANT: VALDES, JAMES J. APPLICANT: MOHYEE, ELDEFRAMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
DEDNESS: double
DGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1641 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
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OTHER INFORMATION:
US-08-792-824-5
                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 87..788
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION:
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                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                            ADDRESSEE:
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CLASSIFICATION:
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100 TGCCTACGGCGGCGGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCGACATCC 159
                     111 AGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAAAACTGTCACCATCACAT 170
                                 171 GTCGAGCAACTGGGAATATTCAAAATTATTAGCATGGTATCAGCAGCACACGGGAAAAT 230
                                                                            CTCCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA 290
                                                                                                                        GTGGCAGTGGATCAGGAACACAATATTCTCTCAGATCAACAGCCTGCAGCCTGAAGATT 350
                                                                                                                                                                    TTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCA 410
                                                                                                                                                                                                                411 AGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTG 470
                                                                                                                                                                                                                                                            471 AGCAGITAACAICTGGAGGIGCCICAGICGIGIGCTICIIGAACAACTICIACCCCAAAG 530
                                                                                                                                                                                                                                                                                                       531 ACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTT 590
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                                                                                                                                                                                                                                                                                                                                                                                                AGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KWAK, JU-WON
APPLICANT: HAN, MOON-HI
APPLICANT: CHOI, BYUNG-KWON
TITLE OF INVENTION: C-DNAS ENCODING MURINE ANTIBODY
TITLE OF INVENTION: AGAINST HUMAN PLASMA APOLIPOPROTEIN B-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/634,783A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 EARLE OVINGTON BLVD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08634783A
Patent No. 5861276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DILWORTH & BARRESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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104 GACATCCAGAIGACTCAGTCTCCAGCCTCCTAICTGCAICTGIGGGAGAAACTGTCACC 163
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                                                                                                                                                                                                                                                                                                                                                             224 GGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                   284 AGGTICAGTGGCAGTGGATCAGGAAÇACAATATTCTCTCAAGATCAACAGCCTGCAGCCT 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 ICCAGIGAGCAGITAACAICIGGAGĢIGCCICAGICGIGIGCIICTIGAACAACIICIAC 523
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                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                        Length 642;
                                                                                                                                                                                                                                                                  78; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.8%; Score 517.2; DB 2;
87.9%; Pred No. 1.6e-115;
                                                                                                                                                                                                                                                              0; Mismatches
                                 25,253
                                          REFERENCE/DOCKET NUMBER: 68
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : Sequence 2, Application US/09070817
; Patent No. 6096516
ATTORNEY/AGENT INFORMATION:
                                                                       516-228-8484
              NAME: BARRESE, ROCCO S. REGISTRATION NUMBER: 25
                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 642 base pairs
                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                   516-228-8516
                                                                                                                                                                                                                                                          564; Conservative
                                                                                                                                                           double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: KWAK, JU-WON
APPLICANT: HAN, MOON-HI
                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                        STRANDEDNESS:
                                                                   TELEPHONE:
                                                                                 TELEFAX:
                                                                                                                                                                                               US-08-634-783A-2
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IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: double
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MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ATCACTIGCAAGGCGAGTCAGGACATITATAGCTATITAAGCTGGTTCCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 GGAAAATCTCCTCAGGTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGGTGCCATCA 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 ATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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            TITLE OF INVENTION: C-DNAS ENCODING MURINE ANTIBODY AGAINST TITLE OF INVENTION: HUMAN PLASMA APOLIPOPROTEIN B-100
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                              333 EARLE OVINGTON BOULEVARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/634,783
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/070,817
                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   DILWORTH & BARRESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGENT INC...
BARRESE, ROCCO S.
BARRESE, TOCCO S.
TOCOMORPHICAL SERVING S.
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TELEPHONE: 516-228-8484
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APPLICANT: CHOI, BYUNG-KWON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                             NUMBER OF SEQUENCES:
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61 ATCACTIGCAAGGCGAGTCAGGACATTAATATCTATTTAAGTIGGTICCAGCAGAAACCA 120
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421 CCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTG 480
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805 Fifteenth Street, N.W., #700
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                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08737129A Patent No. 5885816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheek, Jr.
BER: 33,367
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                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ikuo FUJII et al.
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Oy 284 AGGTTCAG	187	OY 344 GAAGATTTT	Db 247 GAAGATTT		Qy 464 TCCAGTGAG	367	VY 524 CCCAAAGAC	Qy 584 AACAGITGG	487	27 044 TTGACCAAG		Db 607 TCAACTICAG	764	Db 667 GACGCCACCA	RESULT 15 US-09-170-769A-7 Sequence 7, Applicatio Patent No. 6444206 GENERAL INFORMATION: APPLICANT: THE SCRIPP APPLICANT: LETURCO, APPLICANT: TOBIAS, APPLICANT: ULEVITCH, APPLICANT: ULEVITCH, APPLICANT: TOBIAS, TILLE OF INVENTION: M FILE REFERENCE: SCRIP CURRENT APPLICATION IN CURRENT APPLICATION NUM PRIOR FILING DATE: NUMBERR OF SECTION NUM PRIOR FILING DATE: NUMBERR OF SECTION NUM PRIOR FILING DATE: SCRIPPERING DATE: NUMBERR OF SECTION NUM PRIOR FILING DATE: SCRIPPERING DA	; SEQ ID NO 7 ; LENGTH: 633 ; TYPE: DNA ; ORGANISM: Murine	FEATURE: NAME/KEY: CDS OCTHON: (1)(633) OTHER INFORMATION: C	cat i	Matches 539; Conserva QY 113 ATGACTCAGTC	Db 1 ATGACCCAGAC
Db 121 GGGAAATCTCCTAAGGCCTGATCTATCGTACAAACGGATTCTTATTTTTTTT	QY 284 AGGTTCAGTGGCAGTGGGACCACAATATTCTCTCAGAGATCAGGACCTGCAGCTTT 343	181 AGGTTCAGTGGAGTGGATTTGTTGTCTCTCACCATCACCAGCTGGATTTTTTTCTCTCACCAGCAGCAGTATTTTTTTT		OY 404 GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCCACCACAACTTCGGAGGG 300	301 GGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA		524 CCCAAAGACATCAATGTGGAGGTGCCTCAGTGGTGCTTGTTGAACAACTTCTTT 524 CCCAAAGACATCAATGTGAAGAGTGGAAGATTGATGGTAGTAAAGAAAAAAA	Db 421 CCCAAAGACATCAATGTCAAGTGGAAGATTGATGTTTTTTTT		644 TTGACCAAGGACGACGACAACAGCAACAGCACCTACAGCAGCACCCTCACG	Db 541 TIGACCAAGGACGACGATAIGAACGACATAAAGACA 703 541 TIGACCAAGGACGACGATAIGAACGACATAAACAGTAIAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	704 TCAACTTCACCCATGTCAAGAGCTTCAACAGGAATGAGTTA 747	Db 601 TCAACTTCACCCATGTCAAGAGCTTCAACAGGAATGAGTGTTA 644	SSULT 14	5453363-1 ; Patent No. 5453363 APPLICANT: RUDOLPH, RAINER; FISCHER, STEPHAN; MATTES, RALF TITLE OF INVENTION: PROCESS FOR THE ACTIVATION OF T-PA OR INUMBER OF SEQUENCES: 4 NUMBER OF SEQUENCES: 4 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/206,044 FILING DATE: 02-MAR-1994 PRIOR APPLICATION NUMBER: 942,370 FILING DATE: 09-SEP-1592 APPLICATION NUMBER: 498,500 FILING DATE: 23-MR-1990 APPLICATION NUMBER: 76,207 SEQ ID NO:1: LENGTH: 5238		Y 104 GACATCCAGATGACTCAGATCTCCAGCCTCCTATCTGCATCTGTGGGAGAAACTGTCACC 163 b 7 GATATTGTGCTAACTCAGCCACCCTGTTGTGCTCTGAGAGATAGCGTCAGT 66	67 CTTCCTGCAGGCAGCAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAG 223	224 GGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGTGCCATCA 283 1111	

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METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACT
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            STGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCT 343
                                             ITGGGAGTTATTACTGT¢AACATTTTTGGAGTACTCCGTACACGTTCGGAGGG 403
                                                          GCAGTTAACATCTGGAĢGTGCCTCAGTCGTGTTCTTGAACAACTTCTAC 523
                                                                                                                                                      CATCAATGTCAAGTGGÅAGATTGATGGCAGTGAACGACAAAATGGCGTCCTG 583
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                                                                                                                                                                                                                                                                                                                                                'CTCCAGCCTCCCTATCTGCGCAGAAACTGTCACCATCACATGT 172
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85.2%; Pred. No. 3.2e-107;
Live 0; Mismatches 94; Indels 0
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³⁵³ GGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAG 412 241 GCCACTTACTTTGCCAACGGGGTGATACGCTTCCGTGGACGTTCGGTGGAGGCACCAAG 300

⁴¹³ CTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAG 472

³⁰¹ CTGGAAATCAAAAGGGCTGATGCTGCAACTGTATCCATCTTCCCCCATCAGTGAG 360

earch completed: June 24, 2003, 01:22:35 ob time : 55.8675 secs

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	F-	inant antibody; ; antibody engineering; nflammation; therapy; ds. or"
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                                                                                                                                                                                                                                                                                                                                                    code for the heavy chain (AAWI1917) and light chain (AAWI1918) of anti-human interleukin-1 beta (IL-1 beta) murine monoclonal anti-human interleukin-1 beta (IL-1 beta) murine monoclonal antibody (MAD) SK48-E26. They were obtd. from cDNA clones of the heavy and light chains derived from mRNA extracted from SK48-E26 hybridoma cells. They can be used in the prepn. of nucleic acids (see also AAT51438-39) coding for recombinant chimeric and humanised antibodies (see also AAWI1919-20) useful for the treatment and prevention of IL-1 mediated inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid sequences (AAT51436 and AAT51437) respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 751;
                                                                                                                                                                                                                                                 Recombinant and humanised chimeric antibodies against human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                         Hurle MR, Jackson JR, Jonak ZL, Theisen TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 751 BP; 212 A; 186 C; 180 G; 173 T; 0 other;
                                                                                                                                                                                                                                                                   interleukin-1-beta - for preventing and treating interleukin-mediated inflammatory disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 72.4%; Score 708.6; DB 16 Local Similarity 98.8%; Pred. No. 6.9e-135; Local 714; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                   Claim 21; Page 38-39; 62pp; English.
                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                     94US-0206190.
                                                           94WO-US07659.
                                                                                        93US-0090534
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                                                                                                                                                                                                             WPI; 1995-066868/09.
                                                                                                                                                                                                                            P-PSDB; AAW11918.
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W09501997-A1
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626 ATGAGCAGCACCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGT 685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant; region; transform; myeloma cell; light chain; tumour; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen - has murine variable and human constant regions, also DNA encoding it and transformed myeloma cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= T84.12_light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour imaging and immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 15; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ54651 standard; cDNA; 1041 BP.
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T84.12 L4-12-1 light chain.
                                                                                                                                                                  15-JUN-1993;
                                                                                                                                                                                      15-JUN-1992;
                                                                                                                                                  23-DEC-1993
                                                            Synthetic.
                                                                                                                                                                                                                                                Yang YH;
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56 ACTCAGGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATG 115
          116 ACTCAGTCTCCAGCCTCCCTATCTGCATCTGGGAGAAACTGTCACCATCACATGTCGA 175
                                                                            176 GCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCT 235
                                                   236 CAGCICCIGGICIATICIGCAAAAACCITAGCAGAIGGIGIGCCAICAAGGIICAGIGGC 295
                                                                                                                                  226 AAAGCACTGATTTACTCGGCATCCTACCGTTACAGTGGAGTCCCTGATCGCTTCACAGGC 285
                                                                                                                                                      296 AGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGG 355
                                                                                                                                                                   356 AGTTATTACTGTCAACATTTTTGGAG---TACTCCGTACACGTTCGGAGGGGGGACCAAG 412
                                                                                                                                                                                                               346 GAATATTTCTGTCAGCAATGTAACAGCTATCCTCTATTCACGTTCGGCTCGGGGACAACG 405
                                                                                                                                                                                                                                 413 CTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAG 472
                                                                                                                                                                                                                                             CAGITAACAICTGGAGGIGCCTCAGICGIGTGCTTCITGAACAACTICTACCCCAAAGAC 532
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                                                                                                                                                                                                                                                                                                                         593 ACTGATCAGACAGCAAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAG 652
                                                                                                                                                                                                                                                                                                                                                                GACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCA 712
                                                                                                                                                                                                                                                                                                                                                                                                      713 CCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACC 772
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56 ACTCAGGTCCTGGCGTTGCTGCTGCTGCTTACAGGTGCCAGATGTGACATCCAGATG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequences (AAQ54651-52) show the light and heavy chain cDNAs of murine T84.12. The T84.12 antibody is directed against the tumour marker carcinoma embryonic antigen, and is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.8%; Score | 693.4; DB 15; Length 1041; 85.0%; Pred. No. 8.8e-132; tive 0; Mismatches 136; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New chimaeric T84.12 antibody active against carcinoembryonic antigen - has murine variable and human constant regions, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1041 BP; 322 A; 266 C; 213 G; 240 T; 0 other;
                                                                                                                                                                          /product= T84.12_44-12-1_light_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wu A, Yang YHJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding it and transformed myeloma cells
                                                                                                               Location/Qualifiers
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                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                     (CITY ) CITY OF HOPE. (YANG/) YANG Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 1994-007204/01.
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                                                                                                                                                                                                                                                                                                                                                                           833 GACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCTCCTCCTTCTCCTCCTCCTCCTT
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                                                                                                                                                                                                                                                                                        706 CCCATIGICAAGAGCIICAACAGGAAIGAGIGIIAGAGAACAAAGGICCIGAGACGCCACC 765
                                                                                                                                                                                                                                                                                                                    773 ACCAGCTCCCCAGCTCCATCCTATCTTCCCAAAGGTCTTGGAGGCTTCCCCACAAGC 832
 406 TIGGAAAIAAAACGGGCIGAIGCIGCACCAACIGIAICCAICTICCCACCAICCAGIGAG 465
                             473 CAGTTAACATCTGGAGGTGCCTCAGTGGTGCTTCTTGAACAACTTCTAGCCCCAAAGAC 532
                                                       466 CAGITAACATCIGGAGGIGCCICAGICGIGCIICITGAACAACIICIACCCCAAAGAC 525
                                                                                    533 ATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGG 592
                                                                                                                                            593 ACTGATCAGGACAGCAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAG 652
                                                                                                                                                                        586 ACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAG 645
                                                                                                 cDNA insert of pK17G4 encoding kappa anti-carcinoembryonic antigen.
                                                                                                                                                         Immunoglobulin(s) produced by recombinant host cells - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin; ds DNA; carcinoembryonic antigen; vector pK17G4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibodies analogous to forms from mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               953 AAAAAAAAAAAAAAAAAAAAAAAAA 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY ) CITY OF HOPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  676 CIATACCIGIGAGGCCACTCACAAGACAICAACTICACCCATIGICAAGAGCIICAACAG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736 GAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAGCTCCCCAGCTCCATCCTA 795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 CACTCTCACCATTAGCAATGTGCAGTCTGATGACTTGGCAGATATTCTGTCAACAATA 300
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                                                                                                                                                                                                                                                                                                                           601 CTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoglobulin is produced readily in pure monoclonal form. Genetic manipulations can be used to produce chimeras of variants drawing their homology from species differing from each other. Protein
                                                                                                                              Query Match 69.2%; Score 677; DB 5; Length 882; Best Local Similarity 85.7%; Pred. No. 1.9e-128; Matches 752; Conservative 0; Mismatches 125: TnAole
                                                                                                     Sequence 882 BP; 231 A; 243 C; 194 G; 214 T; 0 other;
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RESULT 5

The cDNA is contained within recombinant vector pK1764 and encodes

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XEX

kappa anti-carcinoembryonic antigen chain. Using the vector the

us-03-110-910-3.rng

AAN40023

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436 IGCACCAACTGTATCCATCTTCCCACTCAGTGAGCAGTTAACATCTGGAGGTGCCTC 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX79347 standard; cDNA; 927 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 GCTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The mRNA is the coding sequence of the cDNA fragment contained within recombinant vector pK1/64 (see AAN40022). It encodes kappa anticarcinoembryonic antigen chain. Using the vector the immunoglobulin is produced readily in pure monoclonal form. Genetic manipulations can be used to produce chimeras of variants drawing their homology from species differing from each other. Protein manipulation is also possible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 ATCTGCATCTGTGGGAGAAACTGTCACCATGACATGTCGAGGAAGTGGGGAATATTCAAAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 TIATTIAGCAIGGIAICAGCAGACACAGGGAAAAICTCCTCAGCICCIGGICTAIICIGC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 AAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 TICTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTT 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                376 TTGGAGTACTCCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin(s) produced by recombinant host cells - useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 68.8%; Score 673.8; DB 5; Length 882; Best Local Similarity 64.5%; Pred. No. 8.3e-128; Matches 566; Conservative 184; Mismatches 127; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                    Heyneker HL, Riggs AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 882 BP; 231 A; 244 C; 194 G; 213 U; 0 other;
                                                                                     mRNA encoding kappa anti-carcinoembryonic antigen.
                                                                                                                 Immunoglobulin; ss mRNA; carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibodies analogous to forms from mammals.
                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           Cabilly S, Holmes WE, Wetzel RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig. 3; 79pp; English.
AAN40023 standard; mRNA; 882 BP.
                                                                                                                                                                                                                                                               84EP-0302368
                                                       01-DEC-1991 (first entry)
                                                                                                                                                                                                                                                                                         83US-0483457
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                                                                                                                                                                 1..673
/*tag=
                                                                                                                                                                                                                                                                                                                 (CITY ) CITY OF HOPE. (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1984-283749/46.
                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAP40031.
                                                                                                                                                                                                                                                           06-APR-1984;
                                                                                                                                                                                                                                                                                     08-APR-1983;
                                                                                                                                                                                                                                 14-NOV-1984
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496 AGTCGTGTGCTTCTTGAACAACTT¢TACCCCAAAGACATCAATGTCAAGTGGAAGATTGA 555 556 IGGCAGTGAACGACAAAATGGCGT¢CTGAACAGTTGGACTGATCAGGACAGCAAAGACAG 615 CACCTACAGCATGAGCAGCACCCT¢ACGTTGACCAAGGACGAGTATGAACGACATAACAG 675 676 CTATACCTGTGAGGCCACTCACAAĠACATCAACTTCACCCATTGTCAAGAGCTTCAACAG 735 736 GAATGAGTGTTAGAGACAAAGGTC¢TGAGACGCCACCACCAGCTCCCAGCTCCATCCTA 795 796 ICITCCCITCIAAGGICTIGGAGGCTTCCCCACAAGCGACCIACCACTGTIGCGGIGCIC 855 856 CAAACCTCCCCACCTCCTTCTCPTCCTCCTTTCCTTGGCTTTTAICATGCTAA 915 The invention relates to a method $f \phi r$ inhibiting protein function using Inhibition; function; recombinant; |p21; ras; monoclonal antibody; Inhibiting protein function using recombinant, intracellularly Anti-p21(ras) monoclonal antibody ½13-259 light chain gene. light chain; activity; cancer; neoplasm; oncogene; ds. 916 TATTIGCAGAAAATATTCAATAAAG † GAGTCTTIGCA 952 Claim 9; Column 15-16; 23pp; English

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644 TIGACCAAGGACGAGIAIGAACGACAIAACAGCIAIACCIGIGAGGCCACICACAAGACA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 TIGACCAAGGIIGAATAIGAAAGGCAIAACCICIATACCIGIGAGGIIGIICAIAAGACA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       704 TCAACTICACCCATIGICAAGAGCTICAACAGGAAIGAGIGITAGAGACAAAGGICCIGA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          764 GACGCCACCACCACCTCCCAGCTCCTATCTTCCCTTCTAAGGTCTTGGAGGCTTC 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    721 GGTG---CCACCTGCTCCCAGTTCCTTCCAATCTTCCCTCCTAAGGTCTTGGAGACTTC 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            464 TCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTAC 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524 CCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTG 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  584 AACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 GGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GGGAAATCTCCTCAGCTCCTGATCTATTATGCAAGTAGCTTGCAAGATGGGGTCCCATCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 GAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GACATCCAGATGACACAGTCTCCACATTCCCTGTCTGCATCTCTGGGAGAAACTGTCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 ATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTAGCATGGTATCAGCAGACACAG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACC 163
                                                                                                                                                                                                                                                                                                                                                                                                     44 ATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGT 103
fragments). The protein function to be inhibited is preferably p21(ras). It is especially inhibited by the monoclonal antibody Y13-259. This sequence represents the coding sequence for the light chain of the Y13-259 antibody. The method may be used to inhibit the activity of specific proteins in cells and eliminate undesirable biological responses, e.g. it may be used to treat conditions associated with the over-expression or overactivity of the target protein. In this way the method may be used to treat conditions have the method may be used to treat cancer and neoplasms, by targeting proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 68.2%; Score 667.6; DB 20; Length 927;
Best Local Similarity 84.5%; Pred. No. 1.5e-126;
Matches 789; Conservative 0; Mismatches 134; Indels 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 927 BP; 249 A; 236 C; 203 G; 239 T; 0 other;
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44 AIGAGIGIGCICACICAGGICCIGGCGITGCIGCIGCIGTGGCITACAGGIGCCAGAIGI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCGTTCTGGGGAGAAACTGTCACC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 ATGAGGIGCCTAGCTGAGTTCCTGGGGCTGCTTGTGCTCTGGATCCTTGGAGCCATTGGG 93
                            832 CTCCTTCCTTCGCTTTCATCATGCTAATATTTG--GGGAATATTAAATAAAGTGA 889
884 CICCICCCITICCITIGGCTITIAICAIGCIAAIAITIGCAGAAAAIAITCAAIAAAGIGA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ79929 and AAQ79930 encode AAR66757 and AAR66758, the light and heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transformed plant producing animal-derived anti-virus antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.6%; Score 652; DB 16; Length 961;
82.7%; Pred. No. 2.2e-123;
tive 0; Mismatches 145; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chains of an animal derived anti-tobacco mosaic virus (TWV) chains of an animal derived anti-tobacco mosaic virus (TWV) annoclonal antibody. The cDNAs were incorporated into a finance resultant plant expression vector was used to transform the resultant plant expression vector was used to transform tobacco plants, anking them TMV resistant, the plants could also be biofarmed for the prodn. of anti-virus antibodies.
                                                                                                                                                                                                                                                        Anti-tobacco mosaic virus monoclonal Ab light chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tobacco plants producing anti-tobacco mosaic virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 961 BP; 243 A; 255 C; 213 G; 250 T; 0 other;
                                                                                                                                                                                                                                                                                                 light chain; virus-resistant plants; biofarming; ss.
                                                                                                                                                                                                                                                                                        Tobacco mosaic virus; TMV; monoclonal antibody;
                                                              944 GTCTTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAA 977
                                                                                            890 ATCITIGCACTIGAAAAAAAAAAAAAAAAAAAAAA 923
                       Example 2; Pages 13-14; 26pp; Japanese.
                                                                                                                                                                      AAQ79929 standard; cDNA to mRNA; 961
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 34..753
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Matches 764; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NISB ) JAPAN TOBACCO INC. (KURS ) KURARAY CO LTD.
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94..750
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Socation/Qualifiers 16..735

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/*tag= 16..75

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MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated antigen CA55.1. cDNAs for the heavy (AA094037) and light (AA094036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or V-min humanized 55.1 constructs have been expressed in myeloma
                                                                                                                                                                                                                                                                                                             Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig.16; 121pp; English
                                                                                                                                                                                                                                                Blakey DC, Boot C,
Rose MS, Wright AF;
                                                                                                                                                                                                                                                                              WPI; 1995-215262/28.
                                                                                                                                                                                                                          (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                          cells and E. coli.
                                                                                                                                                                                                                                                                                         P-PSDB; AAR76087
                                                                                                                                                                 29-NOV-1994;
                                                                                                                                                                                                    03-DEC-1993;
                                                                                                                                                                                         03-JUN-1994;
                                                                                                                      WO9515382-A.
                                                                    sig_peptide
                                                                                        mat_peptide
                                                                                                                                                                                                                                           Blakey DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
               Mus sp.
                                     Key
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                     154 Arciccigcaggictagiaagagiciccigcatagiaaiggcaacgcitictigiairigg 213
                                          209 TATCAGCAGACACAGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCA 268
        ----AAAATTATTAGCATGG 208
                                                                                     GATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATC 328
                                                                                                 AACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCG 388
                                                                                                                                                                           TACACGITCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTA 448
                                                                                                                                                                                      449 TCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTGGTGTGTTC 508
                                                                                                                                                                                                                                 ITGAACAACTICTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGA 568
                                                                                                                                                                                                                                                                                                           CAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATG 628
                                                                                                                                                                                                                                                                                                                      AGCAGCACCCTCACGTIGACCAAGGACGAGTATGAACGACATAACAGGTATACCTGTGAG 688
                                                                                                                                                                                                                                                                                                                                                                 GCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAG 748
                                                                                                                                                                                                                                                                                                                                                                                                             AGACAAAGGTCCTGAGACGCCACCACCAGCTCCCAGCTCCATCTTTCCTAA 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCTTGGAGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAACCTCCTCCC 868
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                                                                                                                                                                                                                                                                            164 ATCACATGTCGAGCAAGTGGGAATATTC------
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Hall SM, Paterson DS;

Copley CG,

94WO-GB02610, 94GB-0011089 93GB-0024819.

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GATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTG 158
                                                                                                                                                                                           159 TCACCATCACATGTGGAGCAAGTGGGAATATTC--------AAAATTATT 200
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                                                                                22;
                                     66.5%; Score 650.6; DB 16; Length 952;
83.8%; Pred. No. 4.3e-123;
tive 0; Mişmatches 129; Indels 22;
Sequence 952 BP; 245 A; 268 C; 215 G; 224 T; 0 other;
                                                                      Matches 780; Conservative
                                                    est Local Similarity
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Antigen binding structure; complementarity determining region; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering; humanized antibody; immunotoxin; ss.

AAQ94036 standard; cDNA; 952

AAQ94036;

21-NOV-1995 (first entry) MAb 55.1 light chain cDNA.

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800 CCCTTCTAAGGTCTTGGAGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGCTCCAAA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             860 CCTCCTCCCCACCTCCTTCTCCTCCTCCTTTCCTTGGCTTTTATCATGCTAATATT 919
                                                                                                                                                                                                                                                                                                                                                                               681 CCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATG 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     728 AGIGITAGAGACAAAGGICCIGAGACGCCACCACCAGCICCCAGCICCAICCIAICIIC 787
                                                                                                                                                                                                                                                                                    621 ACAGCATGAGCAGCCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATA 680
                                                                                                                                                                                                                                                                                                                               608 ACAGCATGAGCAGCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATA 667
441 CAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCG 500
                            501 TGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA 560
                                                                                                                    Regulatory element; vector; erythropoietin; growth hormone; insulin; immunoglobulin; bone morphogenetic protein; interferon; interleukin; superoxide dismutase; T-cell receptor; surface membrane protein; viral antigen; transport protein; addressin; regulatory protein; moloney murine leukemia virus; MoMuLV; bovine; alpha-lactalbumin; human; promoter; double mutated pre-mRNA processing enhancer; PPE; encephalomyocarditis virus; ECMV; internal ribosome entry site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Bovine/human alpha-lactalbumin 5' flanking
                                                                                                                                                                                                                                                                                                          IRES; woodchuck mRNA processing enhancer; WPRE; botulinum; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Encephalomyocarditis virus.
Chimeric - Bos sp.
Chimeric - Homo sapiens.
Chimeric - Moloney murine leukemia virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-lactalbumin (LA) Bot vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Clostridium botulinum.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD28310 standard; DNA; 5711 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2093..2336
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/*tag=
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The invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell. The invention further expression of one or more proteins in a host cell. The invention further expression of a protein of interest, comprising providing the host cell transfected with a vector conformation protein of sequence comprising a signal protein and a encoding a polycistronic sequence comprising a signal protein and the desired protein is produced, where the tesignal protein and the desired protein is produced, where the conformant of proteins and vectors of the invention are useful for the Regulatory elements and vectors of the invention are useful for the expression of proteins of interest in a host cell. They are useful for expression of proteins of one or more proteins such as enythropoletin, useful in the expression of one or more proteins such as enythropoletin, useful in the expression of one or more proteins such as enythropoletin, useful in the expression of one or more proteins such as enythropoletin, useful in the expression of one or more proteins such as enythropoletin, useful in the expression of one or more proteins such as enythropoletin, or growth hormones, von Willebrands factor, lung surfactors, form comes, von willebrands factor, interferors, or growth factors, rheumatoid factors, nerve growth factors, or growth factors, rheumatoid factors, interferors for allowing factors, immunotoxins, bone morphogenetic copproteins, osteoinductive factors, immunotoxins, bone morphogenetic copproteins, osteoinductive factors, immunotoxins, bone morphogenetic copprise and simulates, really addressins, required for expressing cortein, interferons, colony stimulating factors, interleukins, supercoiled simulates, really addressins, addressins, required for expressing crantibodies, chimeric proteins and their fragments proteins in mammalian tissue culture host cells, the rectors are useful for expressing comprises the following elements: bovine/human alpha-lactalbumin (LA) Bot vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel regulatory elements including nucleic acid encoding hybrid alpha-lactalbumin promoter or mutant RNA export element, for expressing one or more proteins e.g. antibodies, pharmaceutical proteins in host
                                                                                                                                                                                                                                                                                             "Bot antibody heavy chain Fab coding region"
                                                                                       product= "Bot antibody light chain Fab coding region"
                                                                                                                                                                                                                /product= "Bovine alpha-lactalbumin signal peptide
                             /product= "cc49 signal peptide coding region"
                                                                                                                                                                                                                                                                                                                                                                    /note= "WPRE sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "MOMuLV 3' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 11; 151pp; English.
                                                                                                                                               /*tag= e
/note= "EMCV IRES"
                                                                                                                                                                                                                                               coding region"
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                                                          2444..3088
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2387..2443
                    /*tag= c
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                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bleck GT;
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                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                            CDS
    CDS
                                                                  CDS
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LNBOTDC vector #1.

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cc49 signal peptide, botulinum toxin antibody light chain, IRES from encephalomyocarditis virus (ECMV), bovine alpha-lactalbumin signal peptide, botulinum toxin antibody heavy chain, woodchuck mRNA processing enhancer (WPRE) sequence and 3' moloney murine leukemia virus (MOMULV)
  88888888
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Sequence 5711 BP; 1408 A; 1424 C; 1434 G; 1445 T; 0 other;

Query Match

2401 GGTCTTTCTTCTTCTGTCAGTAACTACAGGTGTCCACTCCGACATCCAGATGACCCA 2460 61 GGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCA 120 121 GTCTCCAGCCTCCCTATCTGCATCTGGGAGAAACTGTCACCATCACATGTCGAGGAAG 180 181 TGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCT 240 CCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGG 300 301 ATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA 360 TTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAAT 420 421 AAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAAC 480 481 ATCTGGAGGTGCCTCAGTGTGTGTTCTTGAACAACTTCTACCCCAAAGACATCAATGT 540 541 CAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCA 600 0; Gaps 64.8%; Score 634.2; DB 24; Length 5711; 90.8%; Pred. No. 1.2e-119; tive 0; Mismatches 68; Indels 0; Matches 675; Conservative Local Similarity 361 δ qq δ 윰 ò q ð g 셤 ò ð a

601 GGACACCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA 660

AD28276

AAD28276 standard; DNA; 6255 BP.

AAD28276;

22-APR-2002 (first entry)

Bovine; alpha-lactalbumin; pharmaceutical; industrial; ECMV; IRES; CMV; encephalomyocarditis virus; diagnóstic; internal ribosome entry site; screening; cytomegalovirus; moloney murine leukemia virus; MoMuLV; /product= "Modified bovine alpha-LA signal peptide 'product= "cc49 signal peptide coding region" /*tag= b /note= "MoMuLV Extended packaging region" /*tag= c /note= "Neomycin resistance gene" /*tag= f /note= "Bot Fab 5 light chain" 'note= "Bot Fab 5 heavy chain" Chimeric - Clostridium botulinum. | Chimeric - Moloney murine leukemia virus. Chimeric - Encephalomyocarditis virus. . d = "CMV promoter" Location/Qualifiers /*tag= a /note= "MoMuLV 5' /*tag= g /note= "EMCV IRES" /note= "MoMuLV 3' coding region" 4874..5572 Chimeric - Bos sp. Chimeric - Cytomegalovirus. ..2306 ..3473 3573..4217 .3572 .4816 υ .4873 659..1468 5662..6255 /*tag= h Chimeric - Unidentified. 589 /*tag= /*tag= 1512. WO200202738-A2 misc_feature misc_feature misc_feature misc_feature misc_feature botulinum; 10-JAN-2002 promoter cdsCDS LTR NEW WENT TO SEE THE SET THE SE

Miller LU, Bleck GT, Bremel RD,

(GALA-) GALA DESIGN INC

29-JUN-2001; 2001WO-US20710. 03-JUL-2000; 2000US-215925P.

Host cell for producing a desired protein and for screening compounds useful for pharmaceutical, industrial, diagnostic and other purposes, comprises multiple integrating vectors having an exogenous gene -WPI; 2002-154737/20.

Example 3; Fig 15; 191pp; English.

The invention relates to a host cell comprising a genome having at least two integrated integrating vectors. The integrating vectors comprise at least one exogenous gene operably linked to a promoter. The host cell is useful for producing a desired protein and for comparing protein functions. The host cells comprises a reporter gene which is from gene fluorescent protein, luciferase, beta-galactosidase and beta-lactamase,

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and the assaying step further comprises detecting a signal from the reporter gene. The desired protein includes proteins for pharmaceutical, industrial, diagnostic and other purposes. The host cells is useful for indirectly detecting the expression of a desired protein, comprising providing the host cell transfected with a vector encoding a providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a desired protein polycistronic sequence comprising a signal protein and the host cell under suitable conditions so that the signal protein and the desired protein is produced, where the presence of signal protein inflicates the presence of desired protein. The present sequence is LNBOTDC vector used in the invention. The vector comprises the following elements: moloney murine leukemia virus (MoMuLV) 5' LTR, MoMuLV extended elements: moloney murine leukemia virus (ECWV), modified bovine alpha-lactalbumin from encephalomyocarditis virus (ECWV), modified bovine alpha-lactalbumin signal peptide coding region, Bot Fab5 heavy chain, and moloney murine leukemia virus (MoMuLV) 3' LTR.
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Sequence 6255 BP; 1433 A; 1741 C; 1607 G; 1474 T; 0 other;

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4190 CAAGAGCTICAACAGGAATGAGTGTTGAAAGCAICGATITCCCCTGAATTCGCCCTCTC 4249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4130 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGT 4189
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGT 720
                                                                                                                                                                                                                                                                                                601 GGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA 660
                                                                                                                                                       481 ATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGT 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 CAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCA 600
                                                                                                   3530 GGICTITCICITCTICTIGICAGIAACIACAGGIGICCACTCCGACAICCAGAIGACCCA 3589
                                                                                                                                                                                                                                                                                                                                                                                                                  361 TTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGGCCAAGGTGGAAAT 420
                                                                                                                                                                                                                                                                               241 CCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGG 300
                                                                                                                                                                                                                                                                                                                                                301 ATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA 360
                                                                                                                                                                                                           181 TGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGGT 240
                                                                 61 GGTCCTGGCGTTGCTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCA 120
                                                                                                                                       121 GICTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAG 180
                                     0; Gaps
Score 634.2; DB 24; Length 6255;
Pred. No. 1.2e-119;
0; Mismatches 68; Indels 0;
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Best Local Similarity 90.8%;
Matches 675; Conservative (
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Bleck GT;

781 CCCAGCTCCATCCTATCTTCCCT 803

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immunoglobulin; bone morphogenetic protein; interferon; interleukin; superoxide dismutase; T-cell receptor; surface membrane protein; ECMV; viral antigen; transport protein; addressin; regulatory protein; IRES; bovine; alpha-lactalbumin; CMV; encephalomyocarditis virus; MOMULV; internal ribosome entry site; cytomegalovirus; botulinum; moloney murine leukemia virus; ds.
                                                                                                                                            Regulatory element; vector; erythropoietin; growth hormone; insulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Modified bovine alpha-LA signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "cc49 signal peptide coding region"
                                                                                                                                                                                                                                                                                                                                                                     **tag= b
roote= "MoMuLV Extended packaging region"
                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "Neomycin resistance gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Bot Fab 5 heavy chain"
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                                                                                                                                                                                                                                                       Chimeric - Moloney murine leukemia virus Chimeric - Bos Sp.
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                                                                                                                                                                                                                                    Chimeric - Encephalomyocarditis virus.
Chimeric - Clostridium botulinum.
                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "MOMuLV 5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= d
/note= "CMV promoter"
        4250 CCTCCCCCCCCTAACGTTACT 4272
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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"EMCV IRES"
AAD28315 standard; DNA; 6255 BP
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4874..5572
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                                                                                                                                                                                                                                                                               Chimeric - Cytomegalovirus. Chimeric - Unidentified.
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                                                                                                            22-APR-2002 (first entry)
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                                                                                                                                LNBOTDC vector #1.
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                                                RESULT 11
                                                           AAD28315
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or - / / o - or o - o - Co

WPI; 2002-154749/20.

Novel regulatory elements including nucleic acid encoding hybrid alpha-lactalbumin promoter or mutant RNA export element, for expressing one or more proteins e.g. antibodies, pharmaceutical proteins in host

Example 3; Fig 16; 151pp; English.

The invention relates to novel regulatory elements and vectors for the expression of one or more proteins in a host cell. The invention further provides methods of indirectly detecting the expression of a protein of providing providing the host cell transfected with a vector desired protein operably linked by an internal ribosome entry site (TRES), and culturing the host cell under suitable conditions so that the signal protein indicates the presence of signal protein indicates the presence of desired protein. CC Regulatory elements and vectors of the invention are useful for the expression of proteins of interest in a host cell. They are useful for the producing an immunoglobulin (19), preferably secretory 19. They are useful for the consecution in the expression of one or more proteins such as erythropolatin, immunoalism is immunosibility. growth hormone, insulin, immunoglobulins, protein C, cytokines and their albumins, DNase, vascular endothelial growth factor, receptors for CD proteins, Osteoinductive factors, nerve growth factors, rheumatoid factors, nerve growth factors, proteins, osteoinductive factors, immunotoxins, bone morphogenetic protein, interferons, colony stimulating factors, interleukins, viral antigens, transport proteins, addressins, regulatory proteins, antibodies, chimeric proteins, addressins, regulatory proteins, particularly useful for expressing G protein coupled receptors and their frammembrane proteins; the retroviral vectors and expressing frammembrane proteins. proteins in mammalian tissue culture host cells, including rat fibroblast cells, bovine kidney cells and human kidney cells. The present sequence is LNBOTOC vector used in the invention. The vector comprises the following elements: moloney murine leukemia virus (MOMULV) 5' LTR, MOMULV extended viral packaging region, neomycin phosphotransferase gene, CMV promoter, cc49 signal peptide coding region, bot Fab 5 light chain, IRES sequence from encephalomyocarditis virus (ECMV), modified bovine alphalactalbumin signal peptide coding region, Bot Fab5 heavy chain and moloney murine leukemia virus (MOMULV) 3' LTR.

Sequence 6255 BP; 1433 A; 1741 C; 1607 G; 1474 T; 0 other;

61 GGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCA 120 Gaps 64.8%; Score 634.2; DB 24; Length 6255; 90.8%; Pred. No. 1.2e-119; 0; 68; Indels Pred. No. 1.2e-119; 0; Mismatches Conservative Local Similarity Matches 675; Query Match

121 GTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAG 180

181 TGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCT 240

241 CCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGG 300

301 ATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA 360

/*tag= f /note= "MoMuLV 3' LTR"

40200202738-A2

10-JAN-2002.

29-JUN-2001; 2001WO-US20710.

361 TTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAAT 420

3950 ATCTGGAGGTGCCTCAGTCGTGGTTCTTGAACAACTTCTACCCCAAAGACATCAATGT 4009 481 ATCTGGAGGTGCCTCAGTCGTGTGĢTTCTTGAACAACTTCTACCCCAAAGACATCAATGT 540 4190 CAAGAGCTICAACAGGAATGAGTGTTGAAAGCATCGATTTCCCCTGAATTCGCCCTCTC 4249 541 CAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCA 600 601 GGACAGCAAAGACAGCACCTACAGGATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA 660 661 TGAACGACATAACAGTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGT 720 721 CAAGAGCTTCAACAGGAATGAGTGT#AGAGACAAAGGTCCTGAGACGCCACCACCAGCTC 780 LSRNL vector; pharmaceutical; industrial; diagnostic; screening; MoMuLV; moloney murine leukemia virus; chimeric; hepatitis B virus; ds. /*tag= e /note= "Neomycin phosphotransferase gene" /*tag= b /note= "Retroviral packaging region" /*tag= c /note= "Hepatitis B|surface antigen" Chimeric - Moloney murine leukemia virus. Chimeric - Unidentified. 4250 CCTCCCCCCCCTAACGTTACT 4272 /*tag= a /note= "MoMuLV 5' LFR" 781 CCCAGCTCCATCTTTCCTT 803 /note= "RSV promoter Location/Qualifiers AAD28272 standard; DNA; 7170 BP. Chimeric - Hepatitis B virus. 22-APR-2002 (first entry) 1034..1714 ..5130 659..897 /*tag= /*tag= . 589 misc_feature misc_feature misc_feature AAD28272; promoter RESULT 12 AAD28272 LTR QΩ ŏ qq á qq δλ qq qq Db ŏ δλ ò

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The invention relates to a host cell comprising a genome having at least two integrated integrating vectors. The integrating vectors comprise at two integrated integrating vectors. The host cell least one exogenous gene operably linked to a promoter. The host cell is useful for producing a desired protein and for comparing protein functions. The host cells comprises a reporter gene which is from gene fluorescent protein, luciferase, beta-galactosidase and beta-lactamase, and the assaying step further comprises detecting a signal from the reporter gene. The desired protein includes proteins for pharmaceutical industrial, diagnostic and other purposes. The host cells is useful for indirectly detecting the expression of a desired protein, comprising providing the host cell transfected with a vector encoding a providing the host cell transfected with a vector encoding a polycistronic sequence comprising a signal protein and a desired protein in produced, where the presence of signal protein and the desired protein is produced, where the presence of signal protein and LSRNL vector used in the invention. The vector comprises the following collections and the signal protein and collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the collections of the colle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2521 TGGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATCTCCTCAGCT 2580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 ATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 GTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGTCCTGGCGTTGCTGCTGCTGCTTACAGGTGCCAGATGTGACATCCAGATGACTCA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        packaging signal, hepatitis B surface antigen; RSV promoter; neomycin phosphotransferase gene and 3' MOMULV LTR.
                                                                                                                                                                                                                                                                                                                                            Host cell for producing a desired protein and for screening compounds useful for pharmaceutical, industrial, diagnostic and other purposes, comprises multiple integrating vectors having an exogenous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.8%; Score 634.2; DB 24; Length 7170; 90.8%; Pred. No. 1.2e-119; tive 0; Mismatches 68; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7170 BP; 1688 A; 1891 C; 1841 G; 1750 T; 0 other;
                                                                                                                                                                           Bremel RD, Miller LU, Bleck GT, York D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 12; 191pp; English.
03-JUL-2000; 2000US-215925P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.89
Matches 675; Conservative
                                                                                       (GALA-) GALA DESIGN INC.
                                                                                                                                                                                                                                                                            WPI; 2002-154737/20
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3061 CAAGAGCTICAACAGGAATGAGTGTTGAAAGCATCGATTTCCCCTGAATTCGCCCCTCTC 3120
                                                                                                                                          2881 CANGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCA 2940
                                                                              This sequence represents the cDNA coding for the light and heavy chain of BotFab 22, a murine recombinant antibody fragment (rFab) specific to botulinum toxin types A and B. A cDNA library was made from mouse mRNA isolated from mice immunised with human pentavalent toxoid. The cloned mouse heavy and light chains were expressed in phage display libraries and screened for their ability to bind to botulinum toxin types A or B. The clones were then isolated and sequenced. Botulinum neurotoxin is produced as several antigenically distinct serotypes (A-G) and is non-covalently associated with non-neurotoxic proteins. The rFab of
                                                                                                                          661 IGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGT 720
                                                                                                                                                                                  721 CAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCACCAG 780
                                                             601 GGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA 660
541 CAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCA 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "BotFab 22 antibody fragment, light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "BotFab 22 antibody fragment, heavy chain"
                 Murine anti-botulinum toxin antibody fragment (BotFab 22) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant antibody fragment; rFab; botulinum; neurotoxin; Clostridium botulinum; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Columns 35-40; 24pp; English.
                                                                                                                                                                                                                                                                                     3121 CCTCCCCCCCCTAACGTTACT 3143
                                                                                                                                                                                                                                                      781 CCCAGCTCCATCCTATCTTCCCT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  AAX86667 standard; cDNA; 1644 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0792824.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rtag= a
/product= '
                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               818..1582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-1997;
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18-02-110-910-3.rng

Recombinant antibody fragment; rFqb; botulinum; neurotoxin;

Clostridium botulinum; detection;

Mus musculus

ds.

Location/Qualifiers

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8888888888888
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neurotoxin complexes A and B. Such antibody fragments are able to act as immunosensors for detecting botulinum toxins in food and are also useful in health care and in military applications. They are less expensive to produce than monoclonal antibodies as they can be isolated from large scale bacterial cultures. Also, the affinity of an read may be altered by mutagenesis of its gene and subsequent screening this invention binds to the non-neurotoxic proteins that are found in

Sequence 1644 BP; 438 A; 446 C; 402 G; 358 T; 0 other;

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51 FGCTCACTCAGGTCCTGGCGTTGCTGCTGTGGGCTTACAGGTGCCAGATGTGACATCC 110
                                                                                 101 receracececececeserserratracrescecaaceaeceresceares 160
                                                                                                            111 AGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACAT 170
                                                                                                                              GTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACAGGGAAAAT 230
                                                                                                                                                                                     CTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA 290
                                                                                                                                                                                                                                                      281 CICCICAGCICCIGGICIATAAIGCAAAACCITAGCAGAIGGIGGCCAICAAGGIICA 340
                                                                                                                                                                                                                                                                                   GTGGCAGTGGATCAGGAACACAATATTCTCTCAGATCAACAGCCTGCAGCCTGAAGATT 350
                                                                                                                                                                                                                                                                                                                                         351 TTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCA 410
                                                                                                                                                                                                                                                                                                   AGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTG 470
                                                                                                                                                                                                                                                                                                                                                                                                                 AGCAGTIAACAICTGGAGGTGCCTCAGTCGTGTGTTCTTGAACAACTTCTACCCCCAAAG 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTT 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCTCACGTTGACCA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
          Length 1644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
                                 50; Indels
 63.9%; Score 626; DB 20;
92.9%; Pred. No. 4.6e-118;
Live 0; Mismatches 50;
                          Matches 656; Conservative
           Best Local Similarity
Query Match
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This sequence represents the cDNA doding for the light and heavy chain of BotFab 5, a murine recombinant antibody fragment (rFab) specific to botulinum toxin types A and B. A cDNA library was made from mouse mRNA isolated from mice immunisade with himman pentavalent toxoid. The cloned mouse heavy and light chains were expressed in phage display libraries of and screened for their ability to bind to botulinum toxin types A or B. The clones were then isolated and sequenced. Botulinum meurotoxin is produced as several antigenically distinct serotypes (A-G) and is conn-covalently associated with non-heurotoxic proteins. The Frab of neurotoxin oranglexes A and B. Such Antibody fragments are able to act as immunosensors for detecting botulinum toxins in food and are also useful in health care and in military applications. They care less expensive to produce than monoclonal antibodies as they can be read and large scale bacterial cultures. Also, the affinity of an refer the corners of the contagenesis of its gene and subsequent screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 IGCTCACTCAGGTCCTGGCGTTGCTGQTGCTGTGGCTTACAGGTGCCAGATGTGACATCC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 TGCCTACGGCGGCGGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCGACATCC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 GTCGAGCAAGTGGGAATATTCAAAATTATTAGCATGGTATCAGCAGACACAGGGAAAAT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 CTCCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                     /product= "BotFab | 5 antibody fragment, light chain"
                                                                                                                                                                                  /product= "BotFab | antibody fragment, heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.9%; Score 626; DB 20; Length 1672;
92.9%; Pred. No. 4.6e-118;
tive 0; Mismatches 50; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1672 BP; 439 A; 452 C; 403 G; 378 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                        Valdes JJ;
                                                                                                                                                                                                                                                                                                                                                                               Burans JP, Eldefrawi ME, Emanuel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Columns 13-18; 24pp; English.
                                                                                                                                                                                                                                                                            97US-0792824.
                                                                                                                                                                                                                                                                                                         96US-0011013.
                                                                                                                                                                                                                                                                                                                       97US-0792824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY30116, AAY30117.
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                                                                                                                                                      847..1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        656; Conservative
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                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                    (USSA ) US SEC OF ARMY.
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                                                                                                                                                                                                                                                                         30-JAN-1997;
                                                                                                                                                                                                                                                                                                      01-FEB-1996;
                                                                                                                                                                                                                                                                                                                       30-JAN-1997;
                                                                                                                                                                                                               US5932449-A.
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                                                                                                                                                    CDS
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qq
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Murine anti-botulinum toxin antibody fragment (BotFab 5) cDNA.

AAX86664 standard; cDNA; 1672

SULT 14

20-OCT-1999 (first entry)

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670 GGACTGATCAGGACAGCAAAGACAGCATCTACAGCATGAGCAGCACCTTCACATTGACCA 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 AGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 GGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an E. coli vector for the heterologous expression of murine recombinant antibody fragments (rFabs) specific to botulinum toxin types A and B. A cDNA library was made from mouse mRNA soluted from mice immunised with human pentavalent toxoid. The
                                                                                                                                                                                                                                                                                                                                                               531 ACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTT 590
                                                                                                                                                                                                                                                                                                                                                                                      351 TTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGACCA 410
                                                                                                                                430 TIGGGAGITATTACTGICAACATTITTGGAGTACTCCGIGGACGITCGGIGGAGCACCA 489
                                                                                                                                                                                                     550 AGCAGITAACATCIGGAGGIGCCICAGICGIGTGCTICITGAACAACTICIACCCCAAAG 609
291 GIGGCAGIGGAICAGGAACACAAIATICICICAAGAICAACAGCCIGGAGCIGAAGAII 350
                                                                                                                                                                                411 AGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTG
                                                                                                                                                                                                                                                                        471 AGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAG
                                                                                                                                                                                                                                                                                                 Murine anti-botulinum toxin rFab bacterial expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          711 CACCCATTGECAAGAGCTTCAACAGGAATGAGTGTTAGAGAGAAAG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant antibody fragment; rFab; botulinum; neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     790 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAATAGCAAGG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum; detection; circular; cyclic; ds.
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                                                                                                                       Claim 29; Columns 9-14; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of botulinum toxin .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX86663 standard; DNA; 4435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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2744 ACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTT 2803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 GGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               651 AGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT 710
                                                                                                                                                                                                                                                                                                                                                                                                                                   471 AGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAG 530
                                                                                                                                                                                                                                                                                                                                                                                 2264 TGCCTACGGCGGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCGACATCC 2323.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               411 AGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCACCATCAGTG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 CTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 TIGGGAGTIATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGGACCA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                 111 AGAIGACICAGICICCAGCCICCCIAICIGCAICIGIGGGAGAAACIGICACCAICACAI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 GTCGAGCAAGTGGGAATATTCAAAATTATTAGCATGGTATCAGCAGACACAGGGAAAAT 230
                                                                                                                                                                                                                                                                                                                                               51 TGCTCACTCAGGTCCTGGCGTTGCTGCTGTGGTGGTTACAGGTGCCAGATGTGACATCC 110
                                                                                                                            act as immunosensors for detecting botulinum toxins in food and they are also useful in health care and in military applications. They are less expensive to produce than monoclonal antibodies as they can be isolated from large scale bacterial cultures. Also, the affinity of an Irea, may be altered by mutagenesis of its gene and subsequent screening
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with non-neurotoxic proteins. The reads of this invention bind to the non-neurotoxic proteins that are found in neurotoxin complexes A and B. The antibody fragments are able to
                                                                                                                                                                                                                                                                                                                    ó
cloned mouse heavy and light chains (AAX86664) were expressed iphage display libraries and screened for their ability to bind to botulinum toxin types A or B. The clones were then isolated and sequenced. Botulinum neurotoxin is produced as several antignically distinct serotypes (A-G) and is non-covalently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    711 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAG 756
                                                                                                                                                                                                                                                                                    Length 4435;
                                                                                                                                                                                                                                                 Sequence 4435 BP; 1163 A; 1124 C; 1110 G; 1038 T; 0 other;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                       63.9%; Score 626; DB 20; 92.9%; Pred. No. 5.2e-118;
                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                            92.9%;
                                                                                                                                                                                                                                                                                                                            Matches 656; Conservative
                                                                                                                                                                                                                            of the expressed rFabs.
                                                                                                                                                                                                                                                                                                            Sest Local Similarity
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Search completed: June 23, 2003, 20:29:09 Job time : 251.227 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

June 23, 2003, 16:26:36 ; Search time 2633.04 Seconds (without alignments) 10820.814 Million cell updates/sec 4109280 Total number of hits satisfying chosen parameters: 2054640 seqs, 14551402878 residues OM nucleic - nucleic search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries IDENTITY_NUC Gapop 10.0 , Gapext 1.0 em_htgo_other:* Minimum DB seq length: 0 Maximum DB seq length: 200000000 em_htg_inv:* em_htg_other:* em_htg_mus:*
em_htg_pln:*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S Description	BC002112 Mus muscu BC019474 Mus muscu BC015292 Mus muscu BC013496 Mus muscu BC013496 Mus muscul BC013496 Mus muscul AF466770 Mus muscul BC013496 Mus musculu BC013496 Mus musculu BC013496 Muscalus BC002035 Mus musculus BC0201781 Mus musculus BC021781 Mus musculus BC021781 Mus musculus BC021781 Musculus BC021781 Musculus BC021781 Musculus BC021781 Musculus BC021781 Musculus BC019760 Mus muscul X87231 Musculus BC019760 Mus muscul X87231 Musculus BC019760 Mus musculus BC019760 Mus musculus AR466768 Mus musculus AR466768 Mus musculus AR4968 Sequence BC018915 Mus musculus AR35993 Sequence AX382153 Sequence	
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% Query Match		
Score	898 811.2 751.8 75	
Result No.	* 1000	

ALIGNMENTS

RESULT 1 BC002112 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	BC002112 Mus musculus, Similar to immunoglobulin kappa chain variable 8 BC002112 BC002112.1 GI:12805290	
SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Strausberg, R., Direct Suhmission	

MMENT

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Contact: amg@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anslation="MSVPTQVLGLLLLWLTDARCDIOMTQSPASLSVSVGETVTITCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASENIYSNLAWYQOKQGKSPQLLVYAATNLADGVPSRFSGSGSGTQYSLTINSLQSED
FGSYYCQHFWGTPFTFGGGTKVGIKRADAAPTVSIFBPSSEQLTSGGASVVCFLNNFY
                                                                                                                                                                                                                                                                                                           through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 7 Row: k Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 ATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 AAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 CICICAAGAICAACAGCCIGCAGCCIGAAGAITIIGGGAGIIAIIACIGICAACAIITIT 377
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                                                                                                                                                                                               Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      web site: http://www_shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (31-JAN-2001) National Institutes of Health, Mammalian
                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome
                                 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                            Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.7%; Score 898; DB 10; 96.3%; Pred. No. 2.1e-238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lone="MGC:6612 IMAGE:3488780"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAH02112.1"
/db_xref="GI:12805291"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/map="C57BL/6J"
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                                                                                                                   Email: cgapbs-r@mail.nih.gov
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ROD 07-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721 ATGAGTGTTAGAGACAAAAGGTCCTGAGACGCCACCACCAGCTCCCAGCTCCTATC 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                      738 ATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACCAGCTCCCCAGCTCCATCCTATC 797
                                                                                                                                                                                                                                                                                                                                                        541 GCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAGACAGCA 600
                                                                                                                                                                                                                                                                                                                                                                                                618 CCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCT 677
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                                                                                                                                                                                                                                                    558 GCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCA 617
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                                                                                                 361 GGGGTACTCCGTTCACATTCGGAGGGGGGACCAAAGTGGGGATAAAACGGGCTGATGCTG 420
                                                                                                                                              438 CACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAG 497
                                                                                                                                                               498 TCGTGTGCTTCTTGAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATG 557
                     301 CCCICACGATCAACAGCCTGCAGTCTGAAGATTTTGGGAGTTATTACTGTCAACATTTT 360
                                                             378 GGAGTACTCCGTACACGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus, clone MGC:28604 IMAGE:4217320, mRNA, complete cds. BC019474
Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                         Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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ACCCTCACGTTGACCAAGGACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACT 694
                                                                                                                                                                                       CACAAGACATCAACTTCACCCATTĠTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAA 754
                                                                                                                                                                                                                                        AGGICCIGAGACGCCACCACCAGCYCCCCAGCTCCTATCTTCCCTTCTAAGGICTT 814
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FGSYYCQHFWDTPFTFGSGTKLEMKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                De Waele, P., Feys, V., Van de Voorde, A., Molemans, F. and Fiers, W. Expression in non-lymphoid dells of mouse recombinant immunoglobulin directed against the tumour marker human placental
                       GGCGTCCTGAACAGTTGGACTGAT¢AGGACAGCAAAGACAGCACCTACAGCATGAGCAGC
                                                                                                                                                                                                                                                                                                                                Mouse mRNA for anti-hPLAP-directed immunoglobulin E6-L chain.
                                                                                                                                                                                                                                                                                                                                                                                                       /note="E6-L chain precursor (AA -20 to 214)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="mature E6|L chain (AA 1-214)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Achieved expression in non lymphoid cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83.9%; Score 821; DB 10;
95.5%; Pred. No. 5.2e-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
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88329081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="E6 hybridoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA31579.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88$ pb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X13187.1 GI:51784
Ig light chain; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="pBRE6L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alkaline phosphatase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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                                                                     Clone distribution: MGC clone distribution information can be found
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FGSYYCQHHSGIPFTFGSGTKLEIKRADAAPTVSIFPPSSEQUTSGGASVVCFLNNFY
PKDINVKNKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MSVPTQVLGLLLCLTGARCDIQLTQSPASLSASVGETVTITCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, Y.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 GCCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 ACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 37 Row: i Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 GTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGC 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CACACAGACATGAGTGTGCCCACTCAGGTCCTGGGGTTGCTGCTGTGTGCTTACAGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 CTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACG 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 CTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATCATTCTGGTATTCCATTCACG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 TTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATC 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            515 AACTICTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAAT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Colon, normal. 5 month old male mouse."
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 CACACAGTCATGAGTGTGCTCACTCAGGTCCTGGCGTTGCTGCTGCTGTGGCTTACAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 CAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAACCTTAGCAGATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 TTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 942;
                                                                                                                                                                                                                                                                                                                                                                                                    /product="Unknown (protein for MGC:28604)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Indels
                                                                                                                                                                                                                                                                           /clone="MGC:28604 IMAGE:4217320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 881.2; DB 10;
Pred. No. 9.8e-234;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 t
                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAH19474.1"
/db_xref="G1:18044485"
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 g
                  Yoon, V.S., Kowis, C.R., 1
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTSTSPIVKSFNRNEC
                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.08;
96.08;
                                                                                                                                                                 identity to protein.
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Matches 90
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Best Local Similarity

ROD 22-MAR-1995

840

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                     Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                   identity to protein
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                          (bases 1 to 959)
                                                       Direct Submission
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                                         Strausberg, R.
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                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 794 TATCTICCCTICTAAGGICITGGAGGCTICCCCACAAGCGACCTACCACTGTIGCGGIGC 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           781 TATCITCCCTTCTAAGGTCTTGGAGGCTTCCCCACAAGCGACCTACCACTGTTGCGGTGC 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 GATGGGAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAGAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCAAC 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACATCTGGAGGTGCC 493
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                                                                                                                                                                                                                                           194 AATTATTTAGCATGGTATCAGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCT 253
                                                                                                                                                                                                                                                             254 GCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAA 313
                                                                                                                                                                                                                                                                                                                                       241 GCGACAAAGTTAGTAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGCACACAG 300
                                                                                                                                                                                                                                                                                                                                                                        314 TATICICICAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACAT 373
                                                                                                                                                                                                                                                                                                                                                                                        374 TTTTGGAGTACTCCGTACACGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGAT 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                              134 CTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGGAATATTCAA 193
                                                                                                                                                                                                          121 CTATCCGTTTCTGTGGGAGAATCTGTCACCATCACATGTCGAGCAAGTGAGAATATTAC 180
                                                                                                            74 CIGCIGCIGIGGCITACAGGIGCCAGAIGIGACAICCAGAIGACICAGICICCAGCCICC 133
                                                                Mus musculus, clone MGC:19136 iMAGE:4216659, mRNA, complete cds.
                                              554 GATGGCAGTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                614 AGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTATGAACGACATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGTCGTGTGCTTCTTGAACAACTTCTACCCCCAAAGACATCAATGTCAAGTGGAAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                              854 TCCAAACCTCCCCCACCTCCTTCTCCTCCTCCTTTCCTT 898
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                  0; Mismatches 40; Indels
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                        Matches 845; Conservative
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DEFINITION

BC015292 RESULT 4

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ACCESSION KEYWORDS

VERSION SOURCE

ORGANISM

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/translation="MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVTISCR
ASQDISNYLMWYQQRPDGTVKLLIYYTSRLYLGVPSRFSGSGSGTDYSLTISNLEQED
IATYFCQQGNTPPFTFGSGTKLEVKRADAAFTVSIFPPSSEQLTSGGASVVCFLNNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 25 Row: g Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 CCAGATGGAACTGTTAAACTCCTGATCTACACATCAAGATTATATTTAGGAGTCCCA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing croup at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 TGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGGAGAAACTGTC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TGTGATATCCAGATGACACACACATCCTCCTCTGTCTGCCTCTCTGGGAGACAGAGTC 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 ACCATCAGTTGCAGGCCAAGTCAGGACATTAGCAATTATTTAAACTGGTATCAGCAGAAA 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
                           Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
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Web site Contact: Gunaratu Yoon, V.: Richards Clone dis through the Series: This clor passed the identity	Location/Qualifiers 1.019		RTSTSPIVKSFNRECT STATE TO STAT	QY 41 GTCATGAGTGGCTCACTCAGGTCCTGGCGTTGCTG DD 17 11 1 1 1 1 1 1 1 1	161	221 CAGGAAATCTCCTCAGCTCCTGGTCTATCTGCAA	341 317 401	Db 377 TCGGGGACAAGTTGGAATAAACGGCTGTTGTTTTTTTTTT
341 CCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGA 400 1		701 ACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTTAGAGGACACACAC		941 TGACTCTTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAA	BC027418 NA Mus musculus, clone MGC:36290 IMAGE:4224032, mRNA, complete cds. BC027418 BC027418-1 GI:20072742	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Strausberg, R. Direct Submission	Submitted (04-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer USA Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: Cganhsfmail.	Tissue Frocurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Sequencing by: Baylor College of Medicine Human Genome Center code: BCM-HGSC

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ibution information can be found
LNL at: http://image.llnl.gov
n: 15
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'SSLHSGVPSRFSGSGSGTHYGLTISNLEPED
DAAPTVSIFPPSSEQLTSGGASVVCFLNNFY
SKDSTYSMSSTLTLTKDEYERHNSYTCEATH
                     X., Hulyk, S.W., Hale, S.M.,
S., Martin, R.G., Muzny, D.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.8%; Score 751.8; DB 10; Length 1038;
89.3%; Pred. No. 9e-198;
                                                                                                                                                                               /product="Unknown (protein for IMAGE:4219618)"
/protein_id="AAH13496.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stanford University School of Medicine, Stanford, CA 94305
http://www-shgc.stanford.edu
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Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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                                                                                                                                                                                                                                                                                                               701 ACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCC 760
                                                                                                                                                                                                                                                                                                                                                                     677 ACATCAACTICACCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCC 736
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                                                                                     581 CTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCTC 640
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                  497 TACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTC
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Mus musculus, clone IMAGE:4219618, mRNA, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            917 TGAGTCTTTGCACTTGACAAAAAAAAAAAAAAAAAAAA 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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Strausberg, R

REFERENCE

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FEATURES

house mouse.

ORGANISM

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ESULT 6 30013496 ACCESSION

KEYWORDS

/ERSION SOURCE 492

447

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	853 CTCCAAACCTCCTCCCACCTCCTTCTCCTCCTTCCTTGGCTTTTATCATGC 912	٥ 	341 00000
	808 CICCAAACTICTCCTCCTCCTCCTCCTCCTCCTTCCTTCGCTTTATCATGC 867	£ dd	
oy da	913 TAATATTGCAGAAAATATTCAATAAAGTGAGTCTTTGCAAAAAAAA	QY	401 GGGGGACCAAGG
Oy 5	973 AAAAAAA 979	qq	398 GGGGGGACCAAG
o qa	 928 Aaaaaa 934	Qy	461 CCATCCAGTGAGG
		ପ୍ର	458 CCATCCAGTGAGC
RESULT 7 AF466770		٥٧	521 TACCCCAAAGACA
LOCUS	AF466770 972 bp mRNA linear ROD 07-FEB-2002 Mus musculus monoclonal antihody RRK-2 licht chois	QQ	518 TACCCCAAAGACA
ACCESSION		QY	581 CTGAACAGTTGGA
VERSION KEYWORDS	AF466770.1 GI:18568341	qq	578 CTGAACAGTTGGA
SOURCE ORGANISM	Mus musculus. Mus musculus	Qy	641 ACGTTGACCAAGG
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scinrogathi, Muriano	qa	638 ACGTTGACCAAGG
KEFERENCE AUTHORS TITE	1 (bases 1 to 972) Lee,U.H., Kwack,K., Park,J.W. and Kwon,B.S.	Å i	701 ACATCAACTICAC
JOURNAL	Submitted (09-JAN-2002) Department of Biological Sciences,	<u>a</u> :	
FEATURES	Location/Qualifiers	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	
DO TROE	/organism="Mus musculus"	g (
Č	/strain="BALB/c" /db_xref="taxon:10090"	δ	821 TTCCCCACAAGCG
SITO O	41745 /note="against human 4-1BB"	Db	818 TTCCCCACAGGG
	/codon_start=1	ολ	881 CICCICCICCITI
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ASE COUNT	271 a 263 c 204 g 231 t 3 others	REGULT 8 MMIG15K	
Query Match	h 76.8%; Score 751.6; DB 10; Length 972.	LOCUS	MMIG15K Mouse mAB-15C5 m
Matches 8	Pred. No. 1e-197; 0; Mismatches 115; Indels	VERSION	X56394 X56394.1 GI:516
У 4	TCCTGGCGTTGCTGTGTTAACACACACAAAAAAAAAAAA	KEYWORDS SOURCE	gamma-immunoglob Mus musculus.
)E q		ORGANISM	Mus musculus Eukaryota; Metaz
у 101	TGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC	REFERENCE AITHORS	Mammalia; Euther 1 (bases 1 to 9)
86 q		TITLE	Vandamme, A.M.1. Direct Submission
7 161 0 158	1 ACCATCACATGTCGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACA 220	E CNG GRASS	Center for Thromb
7 221		AUTHORS	Vandamme, A.M., Bu
3 218	CCAGATGGAACTGTTAAAACTCAGAAAACCTTAGCAGATGGTGCGA 280 CCAGATGGAACTGTTAAAACTCCTGGATCTACACATCAGATTACACTCAGGAGATCCA 277	TITLE	Construction and monoclonal antibo
7 281		MEDLINE PUBMED	Eur. J. Biochem. 91006173 2209622
278	278 TCAAGGTTCAGTGGCAGTGGCTCTGGAACAGATTATTCTCTCACCATTAGGAACCTGGAG 337	COMMENT	rearranged, Zapl;

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TGGGAGTTATTAC‡GTCAACATTTTTGGAGTACTCCGTACACGTTCGGA 400
                                                          GCTGGAAATAAAA¢GGGCTGATGCTGCACCAACTGTATCCATCTTCCCA 460
                SCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTC 520
                                                                                                                                 ATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTC 580
                                                                                                                                                                                           SACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTC 640
                                                                                                                                                                                                                                                      GACGAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAG 700
                                                                                                                                                                                                                                                                                                              CCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCC 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTCCTTGGCTTTTATCATGCTAATATTTGCAGAAAATATTCAATAAAG 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'UI.-1990) Vanddmme A.M.I., University of Leuven,
ombosis and Vaşcular Research, Herestraat 49, B-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d characterization of a recombinant murine
body directed against human fibrin fragment-D dimer
. 192 (3), 767-775 (1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 \Big| \ \mbox{pp} mRNA for immuhoglobulin kappa chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTC 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 CCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 GGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 TCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACAGCCTGCAG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 TATGAAGATGTGGGAGTTTATTATTGTCTACGGTATGATGAGTTTCCATTCACGTTCGGC 361
                                                                                                                                                                                                                                                                                                                                                                                  ASODINSYLSWIOOKPGKSPKTLIYRGNRLVAGVPSRFSGSGSGODYSLTISSLEYED
VGVYYCLRYDEFPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLISGGASVVCFLNNFY
                                                                                                                                                                                                                                                                                                                                                                                                                   PKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 ACCATCACATGTGGAGCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACA 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 CAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 CCAGGGAAATCTCCCTAAGACCCTGATCTACCGTGGAAACAGATTGGTTGCTGGGGGTCCCA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTVTCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 GTCATGAGTGGTCCTCAGGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ACTGICACTICCAAGGCGAGICAGGACATIAATAGCIATITAAGCIGGAICCAGCAGAAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GACATGAGGACCCCTCCTCTTCTTGGAATCTTGTTGCTCTGGTTTCCAGGTATCAAA 61
                    MAISIS directed against crosslinked human fibrin fragment D-dimer Data kindly reviewed (27-NoV-1990) by Vandamme A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is of c DNA corresponding tomRNA for the antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                      /clone="lambda zap kappa(2), lambda gtll-kappa(1)."
/cell_line="hybridoma 1505"
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/tissue_type="plasma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 75.5%; Score 739.6; DB 10; Length 931; al Similarity 87.2%; Pred. No. 2.2e-194; 87.2%; Pred. No. 2.2e-194; 1ndels 0; Mismatches 119; Indels o
                                                                                                                                                                                                                                                           lib="lambda gtll, lambda"
                                                                                                                                                                                                                                                                                               /note="15C5 Ig kappa precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="mature 15C5 Ig kappa"
65. .388
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                                                                                                                                                /db_xref="taxon:10090"
/chromosome="chromosome 12"
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/db_xref="G1:51623"
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389. .706
                                                                                                  /organism-"Mus musculus"
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                                                              .ocation/Qualifiers
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                                                                                                                        strain-"BALB/c'
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CKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEY
EDMGIYYCLQYDEFPRFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNN
FYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      881 CTCCTCCTCCCTTTCCTTGGCTTTTATCATGCTAATATTTGCAGAAAATATTCAATAAAG 940
                                                                                                                                                                                                                                                                                                                                  820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         782 ITCCCCACAAGCGACCIACCACIGIIGCGGIGCICCAAACCICCICCCCACCITCIC 841
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 998)
                                                                                                                                         641 ACGTIGACCAAGGACGAGTAIGAACGACAIAACAGCIAIACCIGIGAGGCCACICACAAG 700
                                                                                                                                                                                                                                       760
                                                                                                                                                                                                                                                                               662 ACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCC 721
                                                                                                                                                                                                                                                                                                                                                     Tonge, D.W., Hennam, J.F., Greene, A.R., Lee, I.D. and Edge, M.D. Cloning and characterization of 1116NS19.9 heavy and light chain cDNAs and expression of antibody fragments in Escherichia coli year Immunol. 7, 56-62 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conceptual translation with partial peptide sequencing;
This sequence comes from Fig. 2"
482 TACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGÄCAAAATGGCGTC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 998 bp mRNA linear PRI 24-NOV-1 anti-colorectal carcinoma light chain=glycoprotein CANAG-50 specific IGG1 kappa [human, 19.9 hybridoma, antibody 1116NS19.9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 138017] from the original journal article. This sequence comes from Fig. 2.
                                             761 TGAGACGCCACCACCACCTCCCATCCTATCTTCCCTTCTAAGGTCTTGGAGGC
                                                                                                                                                                                                                                       701 ACATCAACTTCACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="anti-colorectal carcinoma light chain"
                                                                                                                                                                                                                                                               /gene="anti-colorectal carcinoma light chain"
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/db_xref="taxon:9606"
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ROD 07-MAY-1997 NYLAWYQQQQGKSPRVILYYYKTLVDGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYC QHFWSIPFTFGSGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINV KWKIDGSERQNGVLNSWTQQDSKDSTYSMSSTLTLTKDEYERHNNYTCEATHKTSTSP /translation="VLGLLLLWLTGVRCDIQMTQSPASLSAFVGETVTITCRASGNIH Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinee; Mus 62 GICCIGGCGTIGCIGCIGCIGIGGCTTACAGGIGCCAGAIGIGACAICCAGAIGACICAG 121 122 TCTCCAGCCTCCCTATCTGCATCTGTGGGAAACTGTCACCATCACATGTCGAGCAAGT 181 Mus musculus immunoglobulin rearranged kappa chain mRNA, partial 242 CTGGTCTATTCTGCAAAACCTTAGCÅGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGA 301 302 TCAGGAACACAATATTCTCTCAAGAT¢AACAGCCTGCAGCCTGAAGATTTTGGGAGTTAT 361 362 TACTGICAACATTITIGGAGTACTCCĢIACATGGTGGGGGGGGGGCCAAGCTGGAAAIA 421 2 (bases 1 to 721)
Pajunen,M.1. Saviranta,P., Jauria,P., Karp,M., Pettersson,K., Direct Submission Mantsala,P. and Lovgren,T. | Cloning, sequencing, expression and characterization of three anti-estradiol-17beta Fab fragments
Biochim. Biophys. Acta 1351 (1-2), 192-202 (1997) 182 GGGAATATTCAAAATTATTAGCATG¢TATCAGCAGACACAGGGAAAATCTCCTCAGCTC Pajunen, M., Saviranta, P., Jauria, P., Karp, M., Pettersson, K., 0; Gaps Pajunen, Turku Centre for Submitted (22-APR-1996) M.I. Pajunen, Turku Centre fo Biotechnology, P.O.Box 123, Turku FIN-20521, Finland Location/Qualifiers 70.4%; Score 689; DB 10; Length 721; 97.2%; Pred. No. 2.4e-180; Live 0; Mismatches 20; Indels (linear /cell_line="Hybridþma cell line WIS 8D9" mRNA /product="19 kappa|chain" /protein_id="AAB53777.1" /db_xref="GI:2072139" /product="Ig kappa-chain" /organism="Mus musculus" 721 bp /db_xref="taxon:10090" 168 g /codon_start=1 U56412.1 GI:2072138 (bases 1 to 721) IVKSFNRNEC 173 c Matches 701; Conservative .684 Mus musculus. Mus musculus Similarity 208 a MMU56412 056412 sig_peptide mat_peptide Query Match Best Local DEFINITION source ORGANISM ACCESSION REFERENCE BASE COUNT MMU56412 AUTHORS JOURNAL PUBMED REFERENCE AUTHORS JOURNAL KEYWORDS CDS TITLE ORIGIN 셤 g ŏ δλ g δ g οy

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Direct Submission
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Mantsala,P. and Lovgren,T.
                                                                                                                            Submitted (22-APR-1996) M.I. Pajunen, Turku Centre for Biotechnology, P.O. Box 123, Turku FIN-20521, Finland Location/Qualifiers
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C-region; J-region; V-region; complementarity determining region; framework region; hypervariable region; immunoglobulin light chain; immunoglobulin-kappa; immunoglobulin-kappa subgroup vk-19;
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JOD560 J00552 J00600
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The sequence reported here is a productive rearrangement of myeloma mopc21. The Suttranslated region (5'ut) of the mopc21 myeloma mopc21. The Suttranslated region (5'ut) of the mopc21 followed in that it probably consists of only three bases. Obtained, but based upon other results using the same sequencing correct. This is further supported by the discovery of another kappa v gene which has a 3 bp 5' ut camsigkab. mopc21 has also undergone an unproductive rearrangement camsigkab. The germline variable region of mopc21 has not been sequenced, loci beginning region is j2. [5] reports the comp. strand. See loci beginning camsigkab for rearranged kappa variable regions; see beginning camsigkab for rearranged kappa genes; and see loci regions. In the sites table cdr-complementarity determining region
mouse cdna to myeloma mopc21 mrna; cdna to myeloma p3 (derived from mopc31) mrna; cdna to myeloma mopc149 mrna; cdna to myelomas mopc41a, mcpc603, s107 & hpc76 mrna (see comment).
                                                                                                                                       Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 899 to 943)
Milstein,C., Brownlee,G.G., Cartwright,E.M., Jarvis,J.M. and
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing
Nucleic Acids Res. 9 (18), 4485-4494 (1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamlyn, P.H., Browniee, G.G., Cheng, C.C., Gait, M.J. and Milstein, C. Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
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Immunoglobulin light-chain structural gene sequences cloned in a
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Identical 3' non-coding sequences in five mouse Ig kappa chain
mRNAs favour a unique C kappa gene
Nature 281 (5730), 394-396 (1979)
                                                                                                                                                                                                                                                       Sequence analysis of immunoglobulin light chain messenger RNA
Nature 252 (5482), 354-359 (1974)
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Nature 271 (5645), 582-585 (1978)
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polyA addition site Complete source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 AAACTGCTGATATATGGGGCATCCAACCGGTACACTGGGGTCCCNGATCGCTTCACAGGC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 AGTGGATCAGGAACACAATATTCTCT¢AAGATCAACAGCCTGCAGCCTGAAGATTTTGGG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 AGTIATTACTGTCAACATTTTTGGAG‡ACTCCGTACACGTTCGGAGGGGGACCAAGCTG 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (derived from mopc21 mrna [1],[3]; cdna to myeloma p3 (derived from mopc21) mrna [[2],[5],[6]; cdna to myeloma mopc149 mrna; cdna to myelomas mopc41a, mcpc603, s107 & hpc76 mrna [5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.5e-179;
0; Migmatches 133; Indels 0; Gaps
                                              listed as T in RNA, may be U listed at T in RNA, may be U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="kappa mopc21 mature peptide coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463 TTAACATCTGGAGGTGCCTCAGTCGTGTGTTCTTGAACAACTTCTACCCCAAAGACATC
reading frame variable part
             reading frame joining part reading frame constant part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.0%; Score 685.4; DB 10; Length 943;
                                                                                                                                                                                                                                                                                  /note="kappa mopc2|1 coding sequence"
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                                                                                                                                                                                                                                               /product="kappa mopc21 mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                     NSYTCEATHKTSTSPIVK$FNRNEC"
                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                    /protein_id="AAA38773.1"
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                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:309359"
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412
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5 others

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BCUU2035

Mus musculus, clone MGC:5947 IMAGE:3491358, mRNA, complete cds. BC002035
206 g
                                               69.8%;
85.1%;
255 c
                                                                              763; Conservative
                                                               Local Similarity
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                                                    Query Match
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TISSVQAEDLADYHCGQGXSYPYTFGGGIKLEIKRADAAPIVSIFPPSSEQLISGGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVCFLNNFYPKDINVKWNIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MHQTSMGIKMESQTLVFISILLWLYGADGNIVMTQSPKSMSMSV
                                                                                                                                                                                                                                                                                                                                                                                                                                               ROD 02-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing Nucleic Acids Res. 9 (18), 4485-4494 (1981)
                                                                                                                                                                                                                                                                 836 CTACCACTGTTGCGGTGCTCCAAACCTCCTCCCCACCTCCTTCTCCTCCTCCTCTTTC 895
                                                                                                                                                                                                                                                                                                  823 CTACCACTGTTGCGGTGCTCCAAACCTCCTCCCACCTCCTTCTCCTCCTTTC 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamlyn, P.H., Browniee, G.G., Cheng, C.C., Gait, M.J. and Milstein, C. Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
                                                                                                                                                                                                   776 AGCICCCCAGCICCAICCIAICIICCCIICTAAGGICIIGGAGGCIICCCCACAAGCGAC 835
                                                                                                                                                                                                                   596 GATCAGGACACCAAAGACAGCACCACGATCAGCACCACCTCACGTTGACCAAGGAC 655
                                       583 GATCAGGACAGCAAAGACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGAC 642
                                                                      656 GAGTATGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTTCACCC 715
                                                                                                                                    716 ATTGTCAAGAGCTTCAACAGGAATGAGTGTTAGAGACAAAGGTCCTGAGACGCCACCACC 775
                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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943
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                                                                                                                                                                                                                                                                                   'product "joining region of Ig kappa light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.musculus mRNA for mouse immunoglobulin kappa light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complementary DNA; Ig kappa light chain; immunoglobulin.
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V00810.1 GI:52139
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TITLE

ERSION

4IGK9

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776 AGCTCCCCAGCTCCATCCTATCTTCCCTTCTAAGGTCTTGGAGGCTTCCCCACAAGCGAC 835
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                                                                                                                                                                                                                                                    176 GCAAGTGGGAATATTCAAAATTATTTAGCATGGTATCAGCAGACACACGGAAAATCTCCT 235
                                                                                                                                                                                                                                                                                          163 GCCAGTGAGAATGTGTTACTTATGTTTCNTGGTATCAACAGAAACCAGAGCAGTCTCCT 222
                                                                                56 ACTCAGGTCCTGGCGTTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATG 115
                                                                                                                         43 ACTCTGGTCTTCATATCCATACTGCTCTGGTTATGGAGCTGATGGGAACATTGTAATG 102
                                                                                                                                                                 116 ACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAAAACTGTCACCATCACATGTCGA 175
                                                                                                                                                                                                         103 ACCCAATCTCCCAAATCCATGTCCATGTCAGTAGGAGGAGGGTCACCTTGACCTGCAAG 162
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0
Score 683.8; DB 10; Length 943;
Pred. No. 7e-179;
0; Mismatches 134; Indels 0;
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ROD 07-AUG-2002

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290 AGTGGCAGTGGATCAGGAACACAA†ATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGAT 349
                                                                                                                     AGTGGCAGTGGATCAGGGACAGACTTCACACTCAAGATCAGCAGAGGTGGAGGGTGAGGAT 355
                                                                                                                                                           TTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACACGTTCGGAGGGGGACC 409
                                                                                                                                                                                  AAGCTGGAAATAAAACGGGCTGAT¢CTGCACCAACTGTATCCATCTTCCGACCATCCAGT 469
                                                                                                                                                                                                                                                            470 GAGCAGITAACATCTGGAGGTGCCHCAGTCGTGTGTTCTTGAACAACTTCTACCCCAAA 529
                                                                                                                                                                                                                                                                                                                                      530 GACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCCTGAACAGT 589
                                                                                                                                                                                                                                                                                                                                                                                                                   590 TGGACTGATCAGGACAGCAAAGACACCTACAGCATGAGCAGCACCCTCACGTTGACC 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (24-JUN-1994) K. Janon, Commissariat a l'energie,
atomique, Diep Bat. 152 CEN, Saclay, 91191 Gif/Yvette Cedex, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650 AAGGACGAGTATGAACGACATAACA$CTATACCTGTGAGGCCACTCACAAGACATCAACT 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 830 AGGGACCIACCACIGITGCGGTGCT¢CAAACCTCCTCCCCACCTCCTTCTCCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             836 AGGACCTACCACTGTTGCGGTGCTQCAAACCTCCTCCCACCTCCTTCTCCTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MMMABMST2 974 bp mRNA linear ROD 01
M.musculus mRNA for monoclonal antibody MST2 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kappa light chain; light chain; monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      956 GCACTTGAAAAAAAAAAAAA 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  950 GCAAAAAAAAAAAAAAAAAAA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X79906.1 GI:1556423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
1 (bases 1 to 974)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Janon, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Janon, K
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                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc., Robin Humphreys cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Web site: Canford University School of Medicine, Stanford, CA 94305 Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, Mark) mcd@paxil.stanford.edu Bickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 8 Row: c Column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKLPVRLLVLMFWIPASSSDVVWTQTPLSLPVSLGDQASISCRS
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NNFTPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTC
                                                                                                                                                                       Submitted (31-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 CIGGCGITGCTGCTGCTGTGGCTTACAGGTGCCAGATGTGACATCCAGATGACTCAGTCT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 CIGITGGIGGIGAIGIICIGGAIICCIGCIICCAGCAGIGAIGIIGIGAIGACCCAAACI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 CCACTCTCCCTGCCTGTCAGGTCTAGGGTCCAGCTCCATCTTGCAGATCTAGTCAG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 AATATTCAAAAT-----TATTTAGCATGGTATCAGCAGACACAGGGAAAA 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 CCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTCACCATCACATGTCGAGCAAGTGGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 AGCATTGTACATAGTAATGGAAACACCTATTTAGAATGGTACCTGCAGAAACCAGGCCAG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230 TCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATGGTGTGCCATCAAGGTTC 289
                                                                                                                                                                                                                                                                                          Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 683.6; DB 10; Length 977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 8e-179;
0; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Unknown (protein for MGC:5947)" /protein_id="AAH02035.1"
                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lone="MGC:5947 IMAGE:3491358"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6"
38. .754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:12805155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EATHKTSTSPIVKSFNRNEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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BC002035.1 GI:12805154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="C57BL/6J"
                                                                                                                                                                                                                                                                        Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.88;
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                                                                                                                                     Strausberg, R.
Direct Submission
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                                           house mouse.
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source

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573 ATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGCA 632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            753 AAAGGICCIGAGACGCCACCACCAGCICCCAGCICCAICCIAICTICCCIICIAAGGIC 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 ACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAA 572
                                                                                                                                                                                                                                                                    NFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCE
ATHKTSTSPIVKSPNRNEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333 GCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAGTACTCCGTACA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 CGTTCGGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 CGTTCGGAGGGGGGACCAAGCTGGAAATAAAACGGGCTGATGCTGCACCAACTGTATCCA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 AGCAGACACAGGGAAAATCTCCTCAGCTCCTGGTCTATTCTGCAAAAACCTTAGCAGATG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 AGCAGAAGCCAGGATCCTCCCCCAAACTCTGGATTTATAGCACATCCAACCTGGCTTCTG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 GTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAACA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 CCAGATGTGACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 CCAGAGGACAAATTGTTCTCACCCAGTCTCCAGCAATCATGTCTGCATCTTCTAGGGGAAC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 CTGTCACCATCACATGTCGAGCAAGTGGGAATAT ---TCAAAATTATTAGCATGGTATC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 GGGTCACCATGACCTGCCAGCTCAAGTGTAAGTTCCAGTTACTTGCACTGGTACC 215
                                                                                                                                                                                                                                                                                                                                                  /product="light chain of the monoclonal antibody MST2" 428. .751 /product="light chain of the monoclonal antibody MST2" 275 c 200 g 229 t
                                                                                                                               /product="light chain of the monoclonal antibody MST2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 69.4%; Score 679; DB 10; Length 974; Similarity 86.6%; Pred. No. 1.5e-177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 115;
                                                                                                                                                                                                 /db_xref="SPTREMBL:P80913"
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                                                       /cell_type="hydridomas"
                    /db_xref="taxon:10090"
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                                                                              rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 761; Conservative
                                                                                                                                                                                                                                                                                                                              38. .103
104. .427
                                                                                                                                                                                                                                                                                                                              sig_peptide
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OM protein - protein search, using sw model

Run on:

June 18, 2003, 16:41:53; Search time 33.1938 Seconds (without alignments) 1452.530 Million cell updates/sec

1 MSVLTQVLALLLLMLTGARC......BATHKTSTSPIVKSFNRNEC 234 US-09-770-916-4 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

671580 Total number of hits satisfying chosen parameters: 671580 seqs, 206047115 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

sp_unclassified:* sp_invertebrate:* sp_vertebrate:* sp_rvirus *
sp_bacteriap;* sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:* sp_organelle:* sp_rodent:* Sp_mammal:*
Sp_mhc:* sp_plant:* SP_virus:* SPTREMBL_21:* sp_phage:* Database :

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

Description	Q8vcp0 mus musculu Q8vcp6 mus musculu Q9lw59 mus musculu Q9lwf8 mus musculu Q9lm77 mus musculu Q9m37 mus musculu Q8vc15 mus musculu Q8rc28 mus musculu Q8rc28 mus musculu Q8rc40 homo sapien Q8wt4 homo sapien Q8wt4 homo sapien
SUMMARIES	QBVCPO QBR062 Q91WS9 Q91WPB Q9RA5 Q99M37 Q8VC16 Q8VC16 Q8VC55 Q91W12 Q8RCD0 Q9QFFO Q9QFFO Q9QFFO Q9QFFO Q9QFFO Q9QFFO Q9QFFO Q9QFFO Q9G
DB	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
% Query Match Length DB	234 234 233 234 238 238 239 239 233 233 233 233 233 233 233
% Query Match	91.2 76.6 76.7 76.7 70.2 70.9 70.9 70.9 70.9 70.9 70.9 70.9 70.9
Score	1126 958 946 941 931 886.5 875.5 875.5 668.5 558 437.5
Result No.	13 10 10 11 11 11 11 11 11

61 GKSPQLLVYSAKTLADGVPSRFSGSG\$GTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120

1 MSVLTQVLALLLLMLTGARCDIQMTQ\$PASLSASVGETVTITCRASGNIQNVLAWYQQTQ 60

91.2%; Score 1126; DB 11; Length 234; 92.7%; Pred. No. 1.7e-94; tive 5; Mismatches 12; Indels 0;

Best Local Similarity 92.78 Matches 217; Conservative

δλ q QΥ

Query Match

0; Gaps

426.5 34.6 235 11 402 34.2 236 4 404 32.7 108 4 405.5 32.5 107 4 383.5 30.0 240 4 373.5 30.3 10.7 4 367.29.7 1108 4 360.5 29.2 117 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 134 11 360.5 29.2 109 4 360.5 27.6 109 4 360.5 27.6 100 11 371.5 26.9 241 11 371.5 26.9 241 11 371.5 26.9 107 11 371.5 25.6 109 4 372.5 26.1 107 11 371.5 25.6 109 4 372.5 26.1 107 11 371.5 25.6 109 4 372.5 26.1 107 11 372.5 22.4 114 4	Q90ml1 mus musculu Q96e61 homo sapien O9u177 homo sapien	Q8wuk3 homo sapien Q8wuk3 homo sapien Q9u179 homo sapien Q9u181 homo sapien Q9u181 homo sapien Q9u283 homo sapien Q9u183 homo sapien Q9u185 homo sapien Q9u186 homo sapien Q9u186 homo sapien Q9u178 mus musculu Q9u178 mus musculu Q9u178 mus musculu Q9u10 persy mus musculu Q9u10 mus musculu Q9u10 mus musculu Q9u10 mus musculu Q9u10 mus musculu Q9u10 mus musculu Q9u10 mus musculu Q9u18 mus musculu Q9u180 homo sapien Q9u180 homo sapien Q9u180 homo sapien Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu Q9u180 mus musculu	291045 mus musculu Q9n0w5 oryctolagus
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426.5 34 422 34 404 32 400.5 32 383.95 32 377 30 377 30 377 30 365 29 360.5 29 360.5 29 360.5 29 378 20 378 9.7.7.6	0.1.0.2.7.0.2.8.8.0.4.1.0.0.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2	20	
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, ve 750		d)	Last annotation update)	•	Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi:	NCBI_TaxID=10090; Nodentia; Sciurognathi; Muridae; Murinae; Mus.					mbank/DDBJ databases.										234 AA; 23/UZ MW; 102551C58AC2FA9F CRC64;	
Тяд	1	20, Created)	Last a	п	; Cran.	; Sciu				RMBI //	- 10 C								UNKNOWN_1		1025	
PRELIMINARY;	+ and	(TrEMBLrel 20,	TrEMBLrel. 21,	Mus musculus (Mouse).	ota; Metazoa; Chordata	axID=10090;	CELIENCE EDOM ** .	-COLON:	Strausberg R.;	Submitted (DEC-2001) to the FMBI //pnp. 1.	EMBL; BC019474; AAH19474 1:			O; IPR003006; Ig_MHC.	O; IPR003596; Ig_v.	SMART; SM00409; 1G; 2	SM00407; IGC1; 1.	SM00406; IGV; 1.	_MHC;	ני ני		
RESULT 1 Q8VCP0 ID Q8VCP0	Q8VCP0; 01-MAR-2002	01-MAR-2002	01-JUN-2002 (Hypothetical	Mus mus	Eukaryo Mammali	NCBI_Ta	SEOTEN	TISSUE=COLON:	Strausb	Submitt	EMBL; B(InterPr	InterPro	InterPro	Interpro	SMART; 9	SMART; S	SMART; S	PROSITE;	SECTIFICE))	
RES Q8V ID	A L	DI	덤	os	88	XO N	д 2	RG.	КA	RL	DR.	D.R.	Z i	אַ ה	DR G	DR	DR DR	¥ 6	¥ 3	0	•	(

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Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1
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Matches 180; Conservative
                                                                                                                  Matches 179; Conservative
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                              Hypothetical protein.
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             PROSITE; PS00290;
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                                                                  121 GTKLEIKRADAAPTVSIPPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                               181 NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.6%; Score 958; DB 11; Length 234; 79.5%; Pred. No. 3.3e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC013496; AAH13496.1; -rnterpro: IPR003006: IQ MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC027418; AAH27418.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;
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                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.9 kDa protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                                           PRT; 234 AA
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Matches 182; Conservative
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                                                                                                                                                                                                                                                            131 AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERONGVLNSWTDQDSKD 190
                                                                                                                                                                      71 AKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRAD 130
                                                                                                                                                                                             11 LLLWLTGARCDIOMTQSPASLSASVGETVTITCRASGNIQNYLAWYQOTQGKSPQLLVYS 70
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                Length 233;
                                                                                                                                                                                                                                                                                                                    191 STYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                        29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein. SF029 MW; B0D0B0E6EB7812D2 CRC64; SF0UENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;
SEQUENCE 233 AA; 25781 MW; B1C184DA149A16EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypothetical 25.9 kDa protein.

Mus musculus (Mouse).
                                  Query Match
Best Local Similarity 79.9%; Pred. No. 4.1e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF001TE; PF00047; 19; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 AA
                                                                           16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR001865; Ribosomal_S2.
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Gaps

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63 SPQLLVYSAKTLADGVPSRFSGSG$GTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGT 122
                                                                                                                                                                                                                                                                                                                                                                                                            123 KLEIKRADAAPTVSIFPPSSEQLT$GGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS 182
                                                                                                                                                                                                                                                                                                                                                                                                                               8 LALLLLWLTGARCDIQMTQSPASL$ASVGETVTITCRASGNI-----QNYLAWYQQTQGK 62
                                                                                                                                                                                                                                                                                                    63 SPQLLVYSAKTLADGVPSRFSGSGSGT|QYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGT 122
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 WIDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                             Ouery Match
72.2%; Score 891.5; DB 11; Length 238;
Best Local Similarity 72.4%; Pred. No. 3.8e-73;
Matches 168; Conservative 20; Mismatches 39; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.8%; Score \frac{86.5}{100}; DB 11; Length 238; 72.0%; Pred. No. 1.1e-72; tive 20; Mismatches 40; Indels 5;
                                                                                                                                                                                 238 AA; 26344 MW; FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019760; AAH19760.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.2 kDa protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AA.
                                                                                                                                              PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                             Pfant; PF00047; iq; 2.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
SMART; SM00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003599; 19.
InterPro; IPR003597; 19_c1.
InterPro; IPR003006; 19_MHC.
InterPro; IPR003596; 19_V.
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                                                                                                                                                                 Hypothetical protein.
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Q8VCI6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVSIFPP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
                                                                                                                                                                                              SEQUENCE FROM N.A.
Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
Cloning of cDNAs encoding for anti-White pine blister rust monoclonal
antibody (MaD 7, its light and heavy chains) and construction of a
single chain antibody (scry).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARI52371; AAD40242.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.4%; Score 931; DB 11; Length 214; 81.8%; Pred. No. 8.3e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC002035; AAH02035.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 AA; 23922 MW; 52BA205FDE995E2A CRC64;
                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last Sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 AA.
                                                                                                     Kappa light chain of Mab7 (Fragment).
                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                               SMART, SM00406; IGv. 1.
SMART, SM00410; IG_11ke, 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                             InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; Ig; 2.
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 81.8% 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
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                       09R1A5
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Matches

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Q8R028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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OC OX OX RR RR RR RR RR RR RR DR DR DR DR SQ SQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 QTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LTQVLALLLLWLTGA-RCDIOMTQSPASLSASVGETVTITCRASGNIQN-----YLAWYQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:||:| | || ||||||||||| ::|||: ::|| ||:| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
                                                                                         123 KLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNS 182
                                                                                                                           178 GVLNSWIDQDSKDSTYSMSSTLTLIKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                183 WTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted The EMBL/GenBank/DDBJ databases. Submitted EMBL/GenBank/DDBJ databases. EMBL, BC021781; AAH21781.1; Interpro; IPR003599; Ig. Interpro; IPR003597; Ig.c1. Interpro; IPR003006; Ig_MHC. Interpro; IPR003596; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SFOUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 26.3 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00409; IG; 2.
SM00407; IGc1; 1.
SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                     SULT 8
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Mus musculus (Mouse).

Unknown (protein for MGC:6582).

Eukaryota;

01-MAR-2002 (TrEMBLrel.

QJIMILI; 01-DEC-2001 (TIEMBLIEL: 19, Created) 01-DEC-2001 (TIEMBLIEL: 19, Last sequence update) 01-MAR-2002 (TIEMBLIEL: 20, Last annotation update)

235 AA.

PRT;

PRELIMINARY;

091W12

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121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MLSLAPLESLLLLCVSDSRAETTVTGSPASLSVATGEKVTIRCITSTDIDDDMNWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 GGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNG 178
                                                                                                                                                                                                                                                                                                                                                                                        59 TQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTF 118
                                                                                                                                                                                                                                                                                                              1 MSVŁTQVLALLLIMLTG--ARCDIONTQSPASLSASVGETVTITCRASGNIQNYLAWYQQ 58
                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 NSWIDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VLNSWIDQDSKDSTYSMSSTLTLILTKDEYERHNSYTCEATHKISTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                               3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                       Query Match 70.9%; Score 875.5; DB 11; Length 235; Best Local Similarity 72.0%; Pred. No. 1.1e-71; Matches 170; Conservative 22; Mismatches 41; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.1%; Score 865; DB 11; Length 234; 71.8%; Pred. No. 9.5e-71; tive 18; Mismatches 48; Indels (
                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases Submitted BAC028540; AAH28540.1; -. Hypothetical protein. SEQUENCE 234 AA; 25702 MW; 148377F9C1CD0AEE CRC64;
                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, BC006643, AAH06643.1; InterPro, IPR003006; Ig_MHC.
                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 25.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Watches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=MAMMARY GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                      TISSUE-BREAST TUMOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                  SEQUENCE FROM N.A
                            NCBI_TaxID=10090;
                                                                                                         Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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298 AA; 31867 MW; E0F96B8A17004317 CRC64;
   SEQUENCE
                                Query Match
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SEQUENCE
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                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
                                                                                                                                                                                                         Q920E6
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                                                             δ
                                                                                        q
                                                                                                                     δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                               56 YQQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 YTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSER 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNI-------QNYLAW 55
                                                                                                                                                                                                                                                                                                                                                                                         181 SGNSQESVTEQDSKDSTVSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176 QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                    5; Gaps
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recognizing a cell polarity by using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BALB/C; TISSUB-SPLEEN;
MEDLINE-20183931; PubMed=10706631;
Shinobara N., Demura T., Fukuda H.;
"Isolation of a vascular cell wall-specific monoclonal antibody
                                                                                                                                                                                                                                                                                                                    DB 4; Length 239;
                                                                                                                                                                                                                                                                                                                                               69; Indels
                                                                                                                                                                                                                                Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022362; AAH22362.1; -.
Hypothetical protein.
SEQUENCE 239 AA: 26234 MW; FACEDC3A3B03871D CRC64;
                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                              54.2%; Score 668.5; DB 4
52.7%; Pred. No. 7.3e-53;
tive 39; Mismatches 69
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                                  PRT;
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                                                                                                Hypothetical 26.2 kDa protein.
Homo sapiens (Human).
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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                              PRELIMINARY;
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                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                       Strausberg R.;
                                                                                                                                                                                                         TISSUE=LUNG;
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RESULT 11
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ò g ŏ අ Qγ οp ò Pfam; PF00047; ig; 2. SMART; SM00406; IGv; 2.

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17 GARCDIOMTOSPASLSASVGETVTLTCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLAD 76
                                                                                                                                        21 DIQMTQSPASLSASVGETVTITCRA$GNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarkhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.2%; Score 558; DB 11; Length 298; 89.1%; Pred. No. 1.1e-42; tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.0%; Score 555; DB 11; Length 109; 96.3%; Pred. No. 5.1e-43; tive 2; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF307938; AAL09422.1;
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022823; AAH22823.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 AA; 11943 MW; DADBF98E05DD1501 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 24.9 kDa protein.
                                                                                                                                                                                                                                                                                 109 AA.
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64 PQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHF---WSTPYTFGG 120
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                                                                                                                                                                                                                    119 GGGTKLEI-KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERON 177
                                                                                                                1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                      178 GVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.5%; Score 437.5; DB 4; Length 237; Best Local Similarity 42.6%; Pred. No. 7.4e-32; Matches 100; Conservative 41; Mismatches 83; Indels 11; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                      36.5%; Score 450; DB 4; Length 233; 40.9%; Pred. No. 5.3e-33;
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EMBL, BC022098; AAH22098.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig.AHC.
                                                                   Best Local Similarity 40.9%; Pred. No. 5.3e-33;
Matches 97; Conservative 46; Mismatches 86; Indels
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SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;
233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 24, bkb protein.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 AA.
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SMART; SM00407; IGc1; 1.
SMART; SM00406; IGV; 1.
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KV1G_EUMAN KV1K_EUMAN KV1K_EUMAN KV1K_EUMAN KV4K_EUMAN KV4Z_EUMAN KV1T_EUMAN KV5Z_MOUSE KV5A_MOUSE KV5A_MOUSE	ALIGNMENTS	D; PRT; 115 AA. Created) Last sequence update) Last annotation update)	precursor (Fragment) Craniata; Vertebrat Sciurognathi; Murid	[1] SEQUENCE FROM N.A. MEDLINE-80159999; PubMed-6767723; Nishioka Y., Leder P.; "Organization and complete sequence of identical eplasmacytoma kappa V-region genes."; J. Biol. Chem. 255:3691.3694(1980); -!- MISCELLANBOUGS: THE GENE WAS ISOLATED AND SEQUE TWO DIFFERENT SOURCES, EMBRYOS AND CULTURED PL. THAT SECRETE THE SIMILAR KAPPA CHAIN MOPC 149.	This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as use by non-profit institutions as long as in modified and this statement is not removed. Use entities requires a license agreement (See http or send an email to license@isb.sib.ch).		IG KAPPA CHAIN V-V FRAMEWORK-1. COMPLEMENTARITY-DE: FRAMEWORK-2. COMPLEMENTARITY-DE: FRAMEWORK-3. COMPLEMENTARITY-DE: BY SIMILARITY. 4F41E3D40C539DEC	e 586; DB 1; No. 1.8e-40 ismatches
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1008 1008 1115 1114 1009 1008 1008		FANDAR 01, 01,		SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-8015999; Pubmed-6767723 Nisbiloka Y., Leder P.; "Organization and complete seque plasmacytoma kappa V-region gene J. Biol. Chem. 255:3691-3694(198 -!- MISCELLANEOUS: THE GENE WAS TWO DIFFERENT SOURCES, EMBRY THAT SECRETE THE SIMILAR KAPP	entry is copentry is copentry is copentry in the copentry is copentry in the copentry is a license to license	5.1; Ig_N Ig_v 1.	>120 43 43 54 69 69 108 >115 115 ; 12581	47.5 97.4 vative
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366 362 362 350 350 350 350 350 350 350 350 350		MOUS 5; L-19 L-19	19 Augpa Chain V-V Mus musculus (Mouse Eukaryota, Metazoa; Mammalia, Eutheria; NCBI_TaxID=10090;	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-80159999; I Nishioka Y., Leder "Organization and oplasmacytoma kappa J. Biol. Chem. 255 -!- MISCELLANEOUS: TWO DIFFERENT ETHAT SECRETE TH	This SWISS- Detween the Europea use by no modified ar entities re	EMBL; V00778; CAA2415 PIR; A01918; KVMSK2. HSSP; P01607; IREI. InterPro; IPR003006; DinterPro; IPR005596; Pfam; PF00047; ig; I. SMART; SM00406; IGV; ITMNOGLOBULIN V regis	CHAIN DOMAIN DOMAIN DOMAIN DOMAIN DOMAIN DISULFID NON_TER SEQUENCE	Match Local es 11
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129 ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS 188
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MEDLINE-88329081; PubMed-3138116; de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.; Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Max E.E., Maizel J.V. Jr., Leder P.;
"The nucleotide sequence of a 5.5-kilobase DNA segment containing the mouse kappa immunoglobulin J and C region genes.";
J. Biol. Chem. 256:5116-5120(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altenburger W., Neumaier P.S., Steinmetz M., Zachau H.G.;
"DNA sequence of the constant gene region of the mouse immunoglobulin
                                                                        61 GKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYXCQHFWSTP 115
                                                        61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete sequence of an immunoglobulin mRNA using specific priming and the dideoxynucleotide method of RNA sequencing.";
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete amino acid sequence of a mouse kappa light chain."; Blochem. J. 128:427-444(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamlyn P.H., Brownlee G.G., Cheng C.-C., Gait M.J., Milstein C.; "Complete sequence of constant and 3' noncoding regions of an immunoglobulin mRNA using the dideoxynucleotide method of RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-73008889; Pubmed-5073237;
Svasti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
                                                                                                                                                                                                                                    11-ULL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                   PRT; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND REVISIONS TO 53-59.
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Hamlyn P.H., Gait M.J., Milstein C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biochem. 176:287-295(1988).
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MEDLINE-81191915; PubMed-6262318;
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MEDLINE-73053310; PubMed-4638343;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Svasti J., Milstein C.;
                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         I_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphatase.";
                                                                                                                                                                                                 KAC_MOUSE
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                             modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS 60
non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH A HEAVY CHAIN).; 4B51FF5EF49BAEB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERCHAIN (WITH A HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sheppard H.W., Gutman G.A.; "Albeling forms of rat kappa chain genes: evidence for strong selection at the level of nucleotide sequence."; proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189 KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.0%; Score 481; DB 1; Le
84.0%; Pred. No. 4.2e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.8%; Score 565; DB 1; 1
100.0%; Pred. No. 7.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain; Immunoglobulin C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain C region, A allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 84.0%; Pred. No. 4.2e es 89; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Pred. ....
100.0%; Pred. ....
                                                                                     or send an email to license@isb-sib.ch).
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MEDLINE=82082587; PubMed=6273908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AA; 11778 MW;
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InterPro; IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00047; 1g; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                           EMBL; V00807; CAA24189.1; -.
                                                                                                                                                                                                                                                                         InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106; Conservative
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IGcl; 1.
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                                                                                                                                                                                                                              HSSP; P01842; 7FAB.
MGD; MGI:96495; Igk-C.
                                                                                                                                                                      A02119; K1MS.
S01320; S01320.
                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig;
SMART; SM00407; IGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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KV5D_MOUSE P01636;

SEQUENCE

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129 ADAAPTVSIFPPSSEQLISGGASVVÇFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (WITH A HEAVY CHAIN).
D -> N (IN REF. 2).
N -> K (IN REF. 2).
                                                      Sheppard H.W., Gutman G.A.; "Allelic forms of rat kappa chain genes: evidence for strong selection at the level of nucleotide sequence."; Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The primary structure of a rat kappa Bence Jones protein: phylogenetic relationships of V- and C-region genes.";
J. Immunol. 115:59-62(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.8%; Score 466; DB 1; Length 106
80.2%; Pred. No. 6.6e-31;
tive 13; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4CFA7CA820D1CA36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF. 2).
E -> Q (IN REF. 2).
E -> Q (IN REF. 2).
E -> Q (IN REF. 2).
S -> W (IN REF. 2).
S -> N (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region.
                                                                                                                                 SEQUENCE (BENCE-JONES PROTEIN S211).
                                          MEDLINE=82082587; PubMed=6273908;
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                                                                                                                                                  MEDLINE=75212238; PubMed=807630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 S
11601 MW;
                                                                                                                                                                                                                                                      InterPro; IPR003006; Ig_MHC. InterPro; IPR003597; Ig_c1.
                                                                                                                                                                                                                                                                                                      SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                Starace V., Querinjean P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                 86
106
                                                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1
SMART; SM00407; IGC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                          PIR; A02117; K1RTB.
HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 AA;
            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                             STRAIN-LOU;
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1 ADAAPTVSIFPPSMEQLTSGGATVVCFVNNFYPRDISVKWKIDGSEQRDGVLDSVTDQDS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 DIQMTQSPDYLSASVGETVTITCRASENIXSYLAWYQQKQGKSPQLLVYDAKTLVEGVPS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                              MOI. Immunol. 17:1507-1513(1980).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
PIR; A01919; KVMS49.
                                                                                                                                                                                                                                                                                                                                                     Appella E., Alvarez V.L.; "Amino acid sequence of the variable region of M149 mouse myeloma light chain: comparison with the nucleotide sequence of K2 and K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 KDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                              COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 481; DB 1; Length 108;
Pred. No. 4.3e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12030 MW; 0B5244D2B410D84C CRC64;
                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                          PRT; 108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
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                                                                                                                                                                                                                kappa chain V-V region MOPC 149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c;
MEDLINE=82057806; PubMed=6795447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain C region, B allele.
Rattus norvegicus (Rat).
                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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85.2%;
                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin V region
                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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DISULFID SEQUENCE Query Match

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Best Local

Matches

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Gaps

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DB 1; Length 106;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klobeck H.G., Combriato G., Zachau H.G.; "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Walker precursor.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116; [1]

KACB_RAT

RESULT 5 KACB_RAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klobeck H.G., Combriato G., Zachau H.G.; "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related."; Nucleic Acids Res. 12:6995-7006(1984).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-I REGION WALKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 453; DB 1; Length 129;
; Pred. No. 9.2e-30;
15; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY - DETERMINING - 1.
                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 3
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15-JUL-1999 (Rel. 38, Last annotation update)
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                      FRAMEWORK - 2
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                                                  EMBL; X00965; CAA25477.1; ALT_TERM.
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                                                                                                                                                                                                                                               Immunoglobulin V region; Signal.
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13-AUG-1987 (Rel. 05, Last sequ
                                                                      HSSP; A01883; KIHUWK.
HSSP; P01607; IREI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 GTRLEIK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTKLEIK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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SEQUENCE
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HSSP; P80362; 1WTL. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.

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                                                                                                                                                                                                                                                                                                                                                   1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bentley D.L., Rabbitts T.H.;
"Human immunoglobulin variable region genes -- DNA sequences of two V
kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG KAPPA CHAIN V-I REGION HK102.
                                                      IG KAPPA CHAIN V-I REGION DAUDI
                                                                                                                                                                                                                                   Length 129;
                                                                                 COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                            COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                 COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                 27; Indels
                                                                                                                                                                                                      14235 MW; CAF076BC7E5574C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain V-I region HK102 precursor (Fragment).
                                                                                                                                                                                                                                    35.3%; Score 436; DB 1; 64.6%; Pred. No. 2.1e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-UUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 117 AA.
                                                                                                                                                                                                                                                                 18; Mismatches
                                                                                                                                                                           BY SIMILARITY.
                                                                                                                                                               FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                  FRAMEWORK - 3.
                                                                                                     FRAMEWORK - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=81098966; PubMed=6779204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin V region; Signal.
.Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J00245; AAA59087.1; -. EMBL; Z00001; CAA77292.1; -.
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InterPro; IPR003596; Ig_v.
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Genew; HGNC:5741; IGKV1-5.
                                                                                                                                                                                                                                                    Best Local Similarity 64.69
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 GTKVDNK 129
                                                                                                                                                                                                           129 AA;
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                                                                                                                                                                                                                                                                                       1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-81052342; PubMed-6776411;
Altenburger W., Steinmetz M., Zachau H.G.;
"Functional and non-functional joining in immunoglobulin light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                         61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHF 111
                                                                                                                                                                                                                                                                                                                                                                                              FRAMEWORK - 1.
COMPLEMENTARITY - DETERMINING - 1.
                                                                 COMPLEMENTARITY-DETERMINING-2,
                                                                                                                                                                                                         33.1%; Score 409; DB 1; Length 117; 67.6%; Pred. No. 2.7e-26; Live 19; Mismatches 17; Indels
                                                                                   FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENTARITY - DETERMINING - 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IG KAPPA CHAIN V-V REGION T1.
                                                                                                                   45 110 BY SIMILARITY.
117 117
117 AA: 12768 MW; ADIDF3A40AF1A49B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14385 MW; AFA5563D31BB7E05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%; Score 402; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created) - 21-JUL-1986 (Rel. 01, Last Sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
                                              FRAMEWORK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-V region Il precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAMEWORK - 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; V00772; CAA24150.1; -. PIR; A01920; KVMST1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P80362; 1WTL.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes of a mouse myeloma.";
Nature 287:603-607(1980).
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                            Local Similarity
les 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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NON_TER
SEQUENCE
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SEQUENCE
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61 GKSPQLLVYSAKTLADGVPSRFSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                         1 MSVLTQVLALLLLEWLTGARCDIQMPQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                    21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOPPE-Seyler's Z. Physiol. Chem. $61:1591-1598(1980).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
"Preparative separation of the tryptic hydrolysate of a protein by high-pressure liquid chromatography. The primary structure of a monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Crahiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Indels † 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 RFSGSGSGTEFTLTISSLQPEDFATYFCQQAHSVPLTFGGGTTVDIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 401; DB 1; Length 108;
; Pred. No. 1.1e-25;
19; Mismatches 15; Indels
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Pred. No. 1.1e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMARY; SM00406; IGv; 1.
Immunoglobulin V region; Bence_Jones protein.
                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Wes.
        59.4%; Preq. ....
                                                                                                                                                                                                                                                                    108 AA.
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                           Conservative
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                                                                                                                                                                                                                                                                  STANDARD;
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88
                                                                                                                                                                  121 GTKLEIKR 128
                                                                                                                                                                                           121 GTKLELKR 128
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A01877; K1HUWS.
          Best Local Similarity
Matches 76; Conserv
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SEQUENCE
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CCC DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR ND DR
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-1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
PIR; A01868; KIHUHU.
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"Principle of antibody structure. The primary structure of a monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein Bi). 3. The complete aminno acid sequence and the genetic
                                                                                                                                                                                                                                                                                                                                                   Watanabe S., Hilschmann N.; "The primary structure of a monoclonal kappa-type immunoglobulin L-
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                                                                                                                                                                                                                                                                                                                                                                                              chain of subgroup I (Bence-Jones Protein Hau): subdivision within
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQNYITPTSFGQGTRVEIKR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 399; DB 1; Length 108; Pred. No. 1.6e-25; 8; Mismatches 16; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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                                                      21.JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-I region Hau.
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                                                                                                                                                                                                                                                                                                                   MEDLINE=71032830; PubMed=4097974;
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                                        21-JUL-1986 (Rel. 01, Created)
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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68.5%;
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SMART; SM00406; IGv; 1.
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hes 74; Conserv
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21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
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Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
"The molecular structure of a dimer composed of the variable portions of the Bence-Jones protein REI refined at 2.0-A resolution.";
Biochemistry 14:4943-4952(1975).
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"The primary structure of a crystalline monoclonal immunoglobulin
"The primary structure of a Constance of the protein Rei); isolation
and characterization of the tryptic peptides; the complete amino acid
sequence of the protein; a contribution to the elucidation of the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Immunoglobulin V region; Bence-Jones protein; 3D-structure.
DOMAIN 23
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-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                Immunoglobulin V region; Bence-Jones protein.
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Homo sapiens (Human).
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InterPro; IPR003596; Ig_v.
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                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SMART; SM00406; IGV; 1.
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PDB; 1REI; 17-FEB-84.
                                PIR; A01863; K1HUBI.
HSSP; P01607; 1REI.
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21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                     81 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKR 128
                                                                                                                                                                                                                                                                                                                                                                61 RFSGSGSGTDYTFTISSLQPEDIATYRCQQYQSLPYTFGQGTKLQITR 108
  COMPLEMENTARITY - DETERMINING - 1.
                      COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                            32.0%; Score 395; DB 1; Length 108; 69.4%; Pred. No. 3.2e-25; tive 12; Mismatches 21; Indels
                                       COMPLEMENTARITY-DETERMINING-3.
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11902 MW; 9E8143E1188BCE2A CRC64;
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15-JUL-1999 (Rel. 38, Last annotation update)
                                                FRAMEWORK-4.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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Matches 75; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                               between the Swiss Institute of Bibinformatics and the EMBL outstation
                                                                                                                                                                                                      21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Human immunoglobulin variable region genes -- DNA sequences of two V kappa genes and a pseudogene.";
Nature 288:730-733(1980).
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=83129397; PubMed=6402305;
Bentley D.L., Rabbitts T.H.;
"Evolution of immunoglobulin V genes: evidence indicating that recently duplicated human V kappa sequences have diverged by gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cradiata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catdrrhini; Hominidae; Homo.
                                                                                                                                                                   .
0
                                                                                                                                                                                                                                                                                                81 RFSGSGSGTQYSLKINSLQPEDFG$YYCQHFWSTPYTFGGGTKLEIKR 128
                                                                                                                                                                                                                                                                                                                       IG KAPPA CHAIN V-I REGION HK101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY - DETERMINING - 1.
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                                                                                                              31.8%; Score 392; DB 1; Length 10:
66.7%; Pred No. 5.6e-25;
Live 17; Mismatches 19; Indels
98 107 FRANKHANILY.
23 88 BY SIMILARITY.
108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-I region HK101 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAMEWORK - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-81098966; PubMed=6779204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00406; ĬGv; 1.
Immunoglobulin V region; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01881; K1HU11.
PIR; A21056; A21056.
HSSP; P01607; IREL.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bentley D.L., Rabbitts T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; K01322; AAA58930.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; K01324; AAA58932.1; -. EMBL; V00558; CAA23824.1; -.
                                                                                                                                   Best Local Similarity 66.79
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
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>117
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>117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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0; Gaps
                                                                                                               Query Match 31.8%; Score 392; DB 1; Length 117; Best Local Similarity 66.1%; Pred. No. 6.2e-25; Matches 76; Conservative 15; Mismatches 24; Indels
DISULFID 45 110 BY SIMILARITY.

NON_TER 117 117

SEQUENCE 117 AA; 12799 MW; D7D0FF3718CEF587 CRC64;
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earch completed: June 18, 2003, 16:42:32 ob time : 10.5309 secs

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OM protein - protein search, using sw model

(without alignments)
1316.302 Million cell updates/sec June 18, 2003, 16:41:57 ; Search time 17.0899 Seconds Run on:

US-09-770-916-4 1234

1 MSVLTQVLALLLLWLTGARC........EATHKTSTSPIVKSFNRNEC 234 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq léngth: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Natch 0% Maximum Natch 100% Listing first 45 summaries

Database :

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3 ID	2 2 S0	2 51	2 A3	2 22	2 53	98 3	25	98 ;	PC	. S5	30	S3	. S1	ij	S4	A5	83	82									7	1 6	4 1	CT
	ld di	4	7	0	ι,	ις.	4	80	8	6	6	0	6	6	5	7	0	0	7			5					, r	10	10	10	7
	Lengt	234	234	220	235	225	214	21	21	21	21	240	21	21	22	21	21	230	19	215	21	21	21	22	21	12	-	-	1		77
*	Match Length DB	91.3	78.3	72.8	72.3	72.1	71.9	71.0	70.3	70.3	70.1	6.69	6.69	69.7	69.2	0.69	8.89	60.3	57.1	55.9	55.6	54.3	52.1	51.8	49.6	48.0	47.5	46.9	46.8		7.04
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kanna chain	1	rappa chain	lambda-like	kappa chain	light chain		To happe chain v I	kappa cilain		kappa chain		harry charm	kappa cnain	kappa chain	kanna chain					TA Vappa Chain C r			
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106	108	0 0	223	106	233	107	132	106	9 6	TOR	101	127	1	141	123	129	10	877	106)			
45.8	44.2		C - T -	40.0	40.0	39.3	39.3	39.0		0.60	38.5	3.0		38.4	37.9	37.9		٧٠/٧	37.8				
565	545	נות	710	434	464	485	485	481	101	T 0 #	475	475		4/4	468	468	2 63 7	6.70%	466				
30	31	33	9 (5,5	34	35	36	3.7	30	0 0	39	40		T #	42	43	7.7	* !	45				

S01320 19 kappa chain precursor - mouse C; Species: Mus musculus (house mouse) C; Date: 30-Sep-1989 #sequence_revision C; Accession: S01320 C; Accession: S01320 C; Accession: S01320 C; Accession: S01320 C; Accession: S01320 C; Accession: S01320 C; Accession: S01320 A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobul	RESULT 1 S01320 S01320 Cigar and Superior - mouse Cigar and Superior - Mouse Institute Cigar and Superior - Mouse Institu
A; Accession: S01320 A; Molecule type: mRNA A; Residues: 1-234 <dei> A; Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785 A; Cross-references: EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID:951785 A; Note: this sequence was determined from the differentiated gene C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin F; 1-20/Domain: signal sequence #status predicted <sig> F; 21-234/Product: Ig kappa chain #status predicted <mat> F; 36-110/Domain: immunoglobulin homology <imm></imm></mat></sig></dei>	784; PIDN:CAA31579.1; PID:g51785 m the differentiated gene immunoglobulin homology redicted <sig> predicted <mat>.</mat></sig>

	0;	90	20
	Gaps	WYQQTQ	WYQQKQ (
4 ;	0;	ONYLA	YSNLA
91.3%; Score 1127; DB 2; Length 234; 91.9%; Pred, No. 4.6e-63;	4; Mismatches 15; Indels 0; Gaps	ITCRASGNI	TCRASENI
3.2;	15;	/GETVT	GESVI
1127; DE No. 4.6e	matches	SPASLSASV	SPASLSVSV
Score Pred.	4; Mis	CDIOMTO	сріомто
91.3%;	ative	LLLWLTGAR	LLWLTDAR
Query Match Best Local Similarity	Matches 215; Conservative	1 MSVLTQVLALLLLMLTGARCDIQMTOSPASISASVGETVTITCRASGNIQNYLAWYQOTQ 60	1 MSVPTQVLGLLLLWLTDARCDIQMTQSPASLSVSVGESVTITCRASENIYSNLAWYQQKQ 60
Query Match Best Local S	Matches 2	λ.	å

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111 1 (QQKQ 60	TFGG 120	:111 TFGS 120	NGVL 180	 NGVL 180	34	34
	61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120	61 GKSPQLLVYVATKLVDGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWDTPFTFGS 120	121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180	121 GTKLEMKRADAAPTVSIFPPSSEQL†SGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180	181 NSWIDQDSKDSTYSMSSTLTLIKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234	NSWIDQDSKDSTYSMSSTLTLIKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
MSVPTQVLGLLLLWLTDARCDIQMTQ	GKSPQLLVYSAKTLADGVPSRFSGSG	GKSPQLLVYVATKLVDGVPSRFSGSG	GTKLEIKRADAAPTVSIFPPSSEQLT	GTKLEMKRADAAPTVSIFPPSSEQLT	NSWTDQDSKDSTYSMSSTLTLTKDEY	NSWIDQDSKDSTYSMSSILILIKDEY
1	61	61	121	121	181	181
op,	QY	Db	Qγ	QQ	Qy	Dp

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If Kappa chain precursor (15C5) - mouse C; Species: Mus musculus (house mouse) C; Species: Mus musculus (house mouse) C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 C; Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000 R; Vancacession: S14237 F; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D. Eur. J. Biochem. 192, 767-775, 1990 A; Pitle: Construction and characterization of a recombinant murine monoclonal antibod A; Reference number: S14236; MUID:91006173; PMID:2209622
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RESULT 2

Gaps

Molecule type: mRNA

Query Match

Accession: S14237

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A; Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specifi
                R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 AKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRAD 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKD 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 TQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 KSGTSPKRWIYDTSKLASGVPGRFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 GGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDFQVQIFSFLLISASVIISRGQIVLTQSPAIMSASPGEKVTMTCSASSSVSK-MQWYQQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan.1995 #sequence_revision 06-Jan.1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSVLTQVLALLLLWLTG--ARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255 C; Superfamily: immunoglobulin V region: immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 VLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                       A;Cross-references: EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID:954829 C;Superfamily: immunoglobulin V region; immunoglobulin homology F;38-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72.1%; Score 889.5; DB 2; Length 225; 75.9%; Pred No. 2.1e-48;
                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 SIYSMSSILLLLTKDEYERHNSYTCEATHKISTSPIVKSFNRNEC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        191 STYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                                                                                                       72.3%; Score 892.5; DB 2
73.3%; Pred. No. 1.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                19; Mismatches
                                                  submitted to the EMBL Data Library, July 1992
                                                                                                                                                                                                                                                                                                                                                                                         73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S37483
                                                                                                        A; Reference number: S25057
                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-235 <FIS>
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A; Status: preliminary
A; Molecule type: mRNA
                                                                                                                                          A; Accession: S25058
A; Status: preliminary
C; Accession: S25058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:M23626; GB:J04061; NID:9533234; PIDN:AAA39162.1; PID:9533235:Superfamily: immunoglobulin V region; immunoglobulin homology
Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 ADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIQMTQSPASLSASVGETVTITCRA-----SGNIQNYLAWYQQTQGKSPQLLVYSAKTL 74
                                                                                                                                                                                                                                                                                                                                      1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                            1 MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTVTCKASQDINSYLSWIQQKP 60
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Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Mus musculus (house mouse)
Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 NSWIDQDSKDSTYSMSSTLILIKDEYERHNSYICEATHKISTSPIVKSFNRNEC 234
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                                                                                                                                                                                                                              78.3%; Score 966; DB 2; Length 234; 77.8%; Pred. No. 4.2e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26; Indels
                                                                                                                                                                                                                                                                                 35; Indels
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                                                                                                                                                                                                                                                                                    17; Mismatches
                                                                                                                                                                           36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-96/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g kappa chain V region (17/9) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76.8%;
                                                                                                                                                                                                                                                             77.88;
                                                                                                                                                                                                                                                                                 Matches 182; Conservative
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                                                                   Residues: 1-234 <VAN>
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Molecule type: mRNA

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Accession: A31790

Accession: A31790

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                                                                                              R.Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T. FEBS Lett. 375, 273-276, 1995
A.Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin A.Reference number: S68211; MUID:96085223; PMID:7498516
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A; Residues: 1-218 <AKA>
C; Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porp
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A. Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyn A;Reference number: JC5810; MUID:98063277; PMID:9398605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 ADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ESGVPDRFIGSGSGTDFTLTISTVQAEDLADYFCQQHYSTPYTFGGGTKLEIKRADAAPT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DIQMTQSPASLSASVGETVTITCRA----SGNIQNYLAWYQQTQGKSPQLLVYSAKTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 GVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVS 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 DIQMTQSPASLSASVGETVTITCRASGNIQN----YLAWYQQTQGKSPQLLVYSAKTLAD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig kappa chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody 13-1 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                          6; Gaps
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                                                                                                                                                                                                                                                                                                                C; Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                   22; Indels
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                                                                                                                                                                                                                    A; Status: preliminary; nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                              71.9%; Score 887; DB 2;
79.0%; Pred. No. 2.9e-48;
tive 17; Mismatches 22;
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                                                                                                                                                                                                                                                                    A;Residues: I-214 <TAK>
A;Cross-references: EMBL:D29668
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Best Local Similarity 79.0%
Matches 169; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                            A; Molecule type: mRNA
                                                                             C; Accession: S68212
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If Kappa chain V region (Mabl3-1) - mouse (fragment)

NiAlternate names: immunoglobulin light chain
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: 44-Mug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C; Accession: 568241; 568214
R; Faragai, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Immanka, Submitted to the EMBL Data Library, March 1994
A; Description: Specific peroxidase activity by formation of an antibody L-chain-porph A; Accession: 568241
A; Molecule type: mRNA
A; Rosidues: 1-218 c.TAK>
A; Cross-references: EMBL:D29670; NID:q473962; PIDN:BAR06141.1; PID:q473963
B; Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, FEBS Lett. 375, 273-276, 1995
A; Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr A; Reference number: 568214
A; Reference number: 568214
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C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-densi
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
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A,Accession: PC4203
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Gene 173, 257-259, 1996
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision | 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: immunoglobulin V region | immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 STLTLTKDEYERHNSYTCEATHKT$TSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.3%; Score 867.5; DB 2; 75.3%; Pred. No. 4.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.3%; Score 868; DB 2; 74.8%; Pred No. 4.4e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;113-219/Domain: C region #status predicted <CRG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.88; Pred no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 75.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL:D29670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 'NI', 3-212 <TAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-219 <KWA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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C, Accession: S16112
R; Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D
Rjol. Chem. Hoppe-Seyler 372, 451-453, 1991
A, Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1993
A; Description: Combination of a defined specificity and desired isotype by cloning of
A; Reference number: $38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 DGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 180
                                                                                                                                                                                                                                                                                                                                                                                                                             55 WYQQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWST 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 PYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 RONGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 DIQMTQSPASLSASVGETVTITCRASGNI-----QNYLAWYQQTQGKSPQLLVYSAKTLA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ELVMTQSPLSLSVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGLSPKLLIYIVSNRF 60
                                                                                                                                                                                                                                                          1 MSVLTQVLALLLLMLTGARCDIQMTQSPASLSASVGETVTITCRA-----SGNIQNYLA 54
                                                                                                                                                                                                                                                                                                                         1 MESQTQVLMSLLLWISGTCGDFVMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C;Accession: S38865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:227396; NID:9416538; PIDN:CAA81787.1; PID:9416539 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                              6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 69.9%; Score 862.5; DB 2; Length 219; Best Local Similarity 74.4%; Pred. No. 9.7e-47; Matches 163; Conservative 18; Mismatches 33; Indels 5
                                                                                                                           Length 240;
                                                                                                                                                                                                 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
F;1-20/Domain: signal sequence #status predicted <SIG>F;21-240/Product: Ig kappa chain #status predicted <MAT>F;153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                           Query Match 69.9%; Score 863; DB 2; Best Local Similarity 67.5%; Pred. No. 9.9e-47; Matches 162; Conservative 31; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain V region (G2a) - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kipp, B.; Becker, W.; Schlaak, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig kappa chain - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-219 <KIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S38865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
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Moutalet Acids Res. 17, 7922, 1989
A.Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNA
A.Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain CDNA
A.Reference number: S06084; MUID:90016888; PMID:2508067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yan Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.; ubmitted to the EMBL Data Library, August 1994; Description: Coordinate expression of antibody subunit genes yields high levels of fun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 DGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTNLEIKRADAAPTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 SIFPPSSEQLISGGASVVCFLNNFYPRDINVKWRIDGSERQNGVLNSWIDQDSRDSIYSM 180
                                                                                                                                                                                                                                                                          SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 195
                                                                                                                                            76 DGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTV 135
                                                                                                                                                                                                           61 SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPRTFGGGTKLEIKRADAAPTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 DIQMTQSPASLSASVGETVTITCRASGNI-----QNYLAWYQQTQGKSPQLLVYSAKTLA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DVVMTQSPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRF 60
                DIQMTQSPASLSASVGETVTITCRASGNI-----QNYLAWYQQTQGKSPQLLVYSAKTLA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Mus musculus (house mouse)
Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Cross-references: EMBL:L35138; NID:9522336; PIDN:AAA67525.1; PID:9522337; Superfamily: immunoglobulin V region; immunoglobulin homology; Keywords: heterotetramer; immunoglobulin
                                                                            1 DVLMTQTPLSLPVSLGDQASISCRSSQSIVHTNGNTYLEWYLQKPGQSPKLLIYKVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.1%; Score 864.5; DB 2; Length 219; Best Local Similarity 75.3%; Pred. No. 7.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                            SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-95/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 165; Conservative
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A; Residues: 1-240 <CRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Residues: 1-219 <VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g kappa chain - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
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RESULT 11

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A; Reference number: S16112; MUID:92000313; PMID:1910583

A; Accession: S16112

us-09-770-916-4.rpr

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Search completed: June 18, 2003, 16:47:05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 160; Conservative
                                                                                                                                                                                                                                                 A; Reference number: S42771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                          C; Accession: S42772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                             A; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Species: Jace-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor A;Reference number: JL0029; MUID:88171315; PMID:3127529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132 A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
                                                                                                                                                                                                                                                                                                                                                                              76 DGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 SIFPPSSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 195
                                                                                                                                                                                                                                                                                                                                                                                                            21 DIQMTQSPASLSASVGETVTITCRAS-----GNIQNYLAWYQQTQGKSPQLLVYSAKTLA 75
                                                                                                                                                                                                                                                                                                                             1 DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLYWYLQKPGQSPKPLIYRVSNRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DIQMTQSPASLSASVGETVTITCRASGNI----QNYLAWYQQTQGKSPQLLVYSAKTLA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.7%; Score 860.5; DB 2; Length 219; 74.4%; Pred. No. 1.3e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tch 69.2%; Score 854.5; DB 2; Length 225; al Similarity 74.4%; Pred. No. 3.1e-46; 163; Conservative 15; Mismatches 36; Indels 5;
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-219 <BIT>
C.Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ect except for four positions shown above C; Comment: The protein is an anti-phosphorylcholine antibody. C; Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                         34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 SSTLTLTKDEYERENSYTCEATHKTSTSPIVKSFNRNEC 219
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                                                                                                                          F;16-95/Domain: immunoglobulin homology <IMM>
                                                                                                        C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                           74.48;
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                                                                                                                                                                                                      Best Local Similarity
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Best Local Similarity
Matches 163; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-225 <CHI>
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79 PSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVSIF 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 MTQSPASLSASVGETVTITCRASGNI----QNYLAWYQQTQGKSPQLLVYSAKTLADGV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-217 <SCH->
A;Cross-references: EMEL:X75536; NID:9414143; PIDN:CAA53226.1; PID:9414144
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-93/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.0%; Score 851.5; DB 2; Length 217; 74.1%; Pred No. 4.6e-46; † tive 18; Mismatches 33; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Indels
187 SSTLTLTKDEYERHNSYTCEATHN†STSPIVKSFNRNEC 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 LTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC 217
                                                                                                                                                                                                                                               R;Schellekens, G.A. submitted to the EMBL Data Library, November 1993
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68, Appl 68, Appl 33, Appl 32, Appl 34, Appl 4, Appli 10, Appli 10, Appli 10, Appli 10, Appli 17, Appli 3, Appli 3, Appli 11, Appli 11, Appli 11, Appli 11, Appli 11, Appli	Massachusetts Genera	os 0; tTQ 60 KP 62 GG 120 11 GG 122 VL 180 VL 182
Sequence 68 Sequence 33, Sequence 33, Sequence 30, Sequence 40, Sequence 40, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 10, Sequence 20, Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 20, Sequence 2	ഗ ര	79.8%; Score 985; DB 6; Length 237; Conservative 16; Mismatches 32; Indels 0; Gaps MSVLTOVLALLLLWLTGARCDIOMTOSPASLSASVGETVTITCRASGNIONYLAWYQOTO
PCT-US03-10154-68 US-10-1404-724-68 US-10-1412-406-33 US-10-1412-406-32 US-11-405-027-4346 PCT-US02-27220-4 PCT-US02-27220-4 PCT-US02-27220-1 US-10-123-694-1 US-10-123-694-1 US-10-123-694-1 US-10-123-694-1 US-10-123-694-1 US-10-123-694-1 US-10-123-29-3 US-10-123-29-3 US-10-123-29-3 US-10-124-66-11	ALIGNMENTS 10-219-051B-3411 Gequence 3411, Application US/10219051B Gequence 3411, Application US/10219051B FERREAL INFORMATION: APPLICANT: The General Hospital Corporation doing business APPLICANT: The General Hospital Corporation FILE REFERENCE: Leas 35693 Foreign Countries CURRENT APPLICATION NUMBER: US 60/312,147 FRICA APPLICATION NUMBER: US 60/312,147 FRICA FILING DATE: 2001-08-14 FRICA FILING DATE: 2001-08-14 FRICA FILING DATE: 2001-11-26 FRI	79 8%; Score 985; DB 6; Length 237;
1 PCT-U 6 US-10 6 US-10 6 US-10 6 US-10 6 US-10 1 PCT-U 1 PCT-	ALIGN SULT 1 Sequence 3411, Application US/10219051B Sequence 3411, Application US/10219051B GENERAL INFORMATION: APPLICANT: The General Hospital Corpora APPLICANT: The General Hospital Corpora TITLE OF INVENTION: Nucleotide sequence TILE REPERENCE: Led 35693 Foreign Count CURRENT PELING DATE: 2003-05-09 FRIOR APPLICATION NUMBER: US 60/312,147 PRIOR APPLICATION NUMBER: US 60/312,147 PRIOR PELING DATE: 2001-11-01 PRIOR APPLICATION NUMBER: US 60/346,387 PRIOR FILING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 14715 SOFTWARE: PET SCRIPT LENGTH: 237 TYPE: PRT ORGANISM: Homo sapiens FEATURE: NAMEKEY: misc.feature LOCATION: (1)(237) OTHER INFORMATION: Xaa=Unknown amino a	16; Score 16; Mis 16; Mis 16; Mis 16; Mis 16; Mis 11
8 233 9 4852 9 5 6653 3 235 3 235 1 237 2 237 7 212 7 212 6 214 6 214 8 2214 8 2214 9 237 9 2	A Horizon Hori	79.8%; Conservative 1 TTOVLALLIMITARA "TTOVLALLIMITARA "TTOVLALLIMITARA "TTOVLAYSAKTLADGVI "TTOVLYSAKTLADGVI "TTOVLYSAKTLADGVI "TTOVLYSAKTLADGVI "TTOVLYSAKTLADGVI "TTOVLYSAKTLADGVI "TTOVLYSAKSTI "TTOVLYSAKSTI "TTOVLYSAKSTI "TTOVLYSAKSTI
762 61.8 762 61.8 759 61.7 759 61.7 759 61.5 61.5 61.3 6.5 61.3 751 60.9 751 60.9 751 60.9 751 60.9 749 60.7 748 60.6 748 60.6 748 60.6	1B-3411 411, Applice FCRMATION: FTHE GENERATION: FORWATION: HOSPITED INVENTION: FELICATION NUM ING DATE: ACTOR DAT	
227 229 330 331 331 332 333 333 334 444 441 77 444 77 77 77 77 77 77 77 77 77 77 77	RESULT 1 Sequence 3411, Application US/10215 SEQUENCE 3411, Application US/10215 GENERAL INFORMATION: APPLICANT: The General Hospital CC APPLICANT: Hospital / Bayer AG TITLE OF INVENTION: Nucleotide sec FILE REFERENCE: Lea 35693 Foreign CURRENT APPLICATION NUMBER: US/10/ CURRENT FILING DATE: 2001-05-09 PRIOR FILING DATE: 2001-08-14 PRIOR FILING DATE: 2001-11-26 PRIOR FILING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 14715 SOFTWARE: PAT SCAPICATION NUMBER: US 60/33 PRIOR FILING DATE: 2001-11-26 NUMBER OF SEQ ID NOS: 14715 SEQ ID NO 3411 LENGTH: 237 CREATURE: NAME/KEY: misc_feature LCCATION: (1)(237) OTHER INFORMATION: Xaa=Unknown ammis-10-10-10-10-10-10-10-10-10-10-10-10-10-	Query Match Best Local (Matches 18) 3 3 3 61 61 61 61 121 121 123 183
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LENGTH: 237

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117 TFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                    123 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 182
                                                                                                                                                                                                                                                                                                     61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
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                                                                                                                                                                                                                           1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Ikuko
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
                                                                                                                                                   0; Gaps
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                                                                                               Length 237;
                                                                                            79.8%; Score 985; DB 6; Length 23:
79.5%; Pred. No. 2.3e-78;
tive 16; Mismatches 32; Indels
LOCATION: (1)..(237)
OTHER INFORMATION: Xaa=Unknown amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10384933 GENERAL INFORMATION:
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Best Local Similarity
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                                                  US-10-219-051B-14374
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                                                                                                            APPLICANT: The General Hospital Corporation doing business as Massachusetts General
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79.8%; Score 985; DB 6; Length 237;
Best Local Similarity 79.5%; Pred. No. 2.3e-78;
Matches 186; Conservative 16; Mismatches 32; Indels
                                                                                                                              APPLICANT: Hospital / Bayer AG
TITLE OF INVENTION: Nuclectide sequences involved in pain
FILE REPERENCE: LeA 3563 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/219,051B
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: US 60/312,147
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-01
PRIOR PRICATION NUMBER: US 60/333,347
PRIOR PRICATION NUMBER: US 60/333,347
PRIOR PRICATION NUMBER: US 60/333,347
PRIOR PRICATION NUMBER: US 60/333,347
PRIOR PRICATION NUMBER: US 60/333,347
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LOCATION: (1)...(237)
OTHER INFORMATION: Xaa=Unknown amino acid
is-10-219-051B-12786
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PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/346,382
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/333,347
PRIOR FILING DATE: 2001-11-26
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                                                       Sequence 12786, Application US/10219051B GENERAL INFORMATION:
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SOFTWARE: Perl script
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Perl script
SEQ ID NO 12786
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OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct
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APPLICANT: Kimborly, Robert P.
APPLICANT: Kimborly, Robert P.
APPLICANT: Kopman, William J.
APPLICANT: LoBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
TITLE OF INVENTION: APOPTOSIS-INDUGING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0029P2
CURRENT APPLICATION NUMBER: PCT/US02/35333A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 KSPQLLVYSAKTLADGVPSRFSGS¢SGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGG 121
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73.4%; Pred. No. 2.7e-69;
tive 20; Mismatches 41; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                          41; Indels
                                                                                                                                                                                                                                                                   71.4%; Score 881.5; DB 1, 73.4%; Pred No. 2.7e-69; tive 20; Mismatches 41;
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PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/201/14151
PRIOR FILING DATE: 2001-05-02
PRIOR PELICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
PRIOR FILING DATE: 2000-05-02
SOFTWARE: PatentIn version 3.0
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                                       SOFTWARE: Patentin version 3.0
                                                                                                                                             ORGANISM: Artificial Sequence
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             NUMBER OF SEQ ID NOS: 102
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Matches 171; Conservat
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Best Local Similarity
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LENGTH: 234
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                                                                                                                        APPLICANT: TOBIAS, Peter S.
APPLICANT: MATHISON, John C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVATILE REFERENCE: SCRIPL140-4
CURRENT APPLICATION NUMBER: US/10/236,051
CURRENT FILING DATE: 2002-12-13
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APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS FACTOR-
TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERAPEUTIC AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 GSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVSIFPPSSE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTK 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 73.5%; Score 907; DB 6; Length 211; Best Local Similarity 81.0%; Pred. No. 1.4e-71; Matches 171; Conservative 18; Mismatches 22; Indels
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CURRENT APPLICATION NUMBER: PCT/US02/34420A
CURRENT FILING DATE: 2002-10-25
PRIOR APPLICATION NUMBER: 60/391,478
                    APPLICANT: THE SCRIPPS RESEARCH INSTITUTE APPLICANT: LETURCO, Didier J.
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 09/170,769
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 08/373,297
PRIOR FILING DATE: 1995-01-23
PRIOR APPLICATION NUMBER: PCT/US94/05898
PRIOR FILING DATE: 1994-05-27
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PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 08/070,160
PRIOR FILING DATE: 1993-05-28
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PRIOR APPLICATION NUMBER: 60/346,402
                                                                           MORIARTY, Ann M.
ULEVITCH, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Koopman, William J. APPLICANT: Oshumi, Jun
                                                      LETURCQ, Didier J.
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APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity
GENERAL INFORMATION:
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                                                                                                      APPLICANT:
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SEQ ID NOS: 102
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LENGTH: 234
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LENGTH: 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LOBUGILO, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF FILE REFERENCE: 21085.002907
CURRENT APPLICATION NUMBER: US/10/286,132A
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US 60/346,402
                                                                       122 TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN 181
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63 QSPKLLIYWASTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCQQY-SSYRTFGGG 121
                                             122 TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERONGVLN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102
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                                                                                                                                                                                                                                                                                                                          Sequence 24, Application US/10286132A
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Oshumi, Jun
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhou, Tong APPLICANT: Kimberly, Robert P.
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Kimberly, Robert P.
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                                                                                                                                                                                                                                                                                                     JS-10-286-132A-24
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APPLICANT: Zhou, Tong
APPLICANT: Lihikawa, Kimihisa
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOP
TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
FILE REFERENCE: 21085.0023U5
CURRENT APPLICATION NUMBER: US/10/275,180A
CURRENT FILING DATE: 2002-10-31
APPLICANT: Buchsbaum, Donald J.

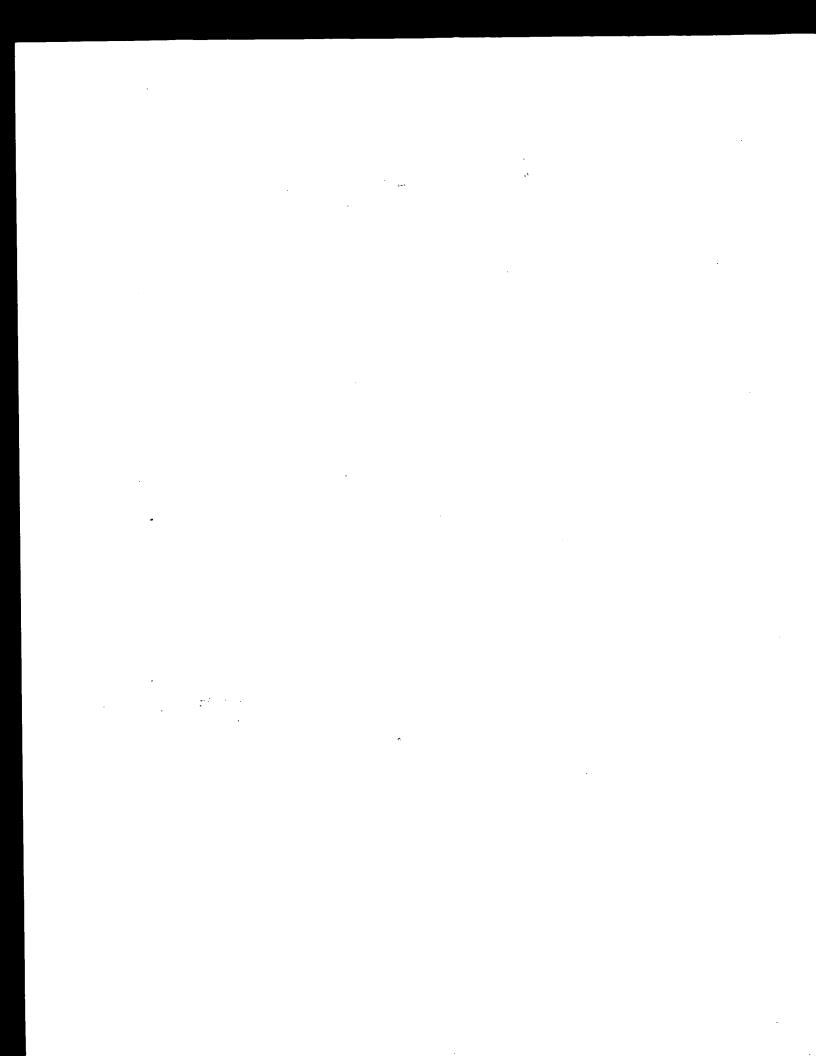
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER T
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 21085.0029u6
CURRENT APPLICATION NUMBER: US/10/281,479A
PRIOR APPLICATION NUMBER: 60/391,478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence:/Note = Synthetic Construct US-10-281-479A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 TKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLN 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.4%; Score 881.5; DB 6; Length 234; Best Local Similarity 73.4%; Pred. No. 2.7e-69; Matches 171; Conservative 20; Mismatches 41; Indels 1:
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                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION UNMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
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PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
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	Matches 169; Conservative 17; Mismatches 43; In	Indels 0; Gaps 0;
QY 2 SVLTQVLALLIMITGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQG 61	QY 5 TQVLALLLMLTGARCDIQMTQSPASLSASVGETVTITCRASGNIONYLAWYQQTQGKSP	
	655	
	125	
OY 182 SWTDQDSKDSTYSMSSTLTLTRDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234	185	NAVUNALGSGUSGESVI 186 PENRNE 233
ation US/09726219A a Antibody Technology Besearch Council tty, John Tthony Ttkony Tkevin Dom, Hendricus Tkevin Thony Tinchony Tinchony Tinchony Tinchony Tinchony Tinchony Tinchony Tinchon Tinchony Tinchony Tinchon Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Gragory Tinchon Towid Tinchon Towid Tinchon Towid Tinchon Towid Tinchon Towid Tinchon Towid Tinchon Towid Tinchon Towid Tinchon Towid Tinchon Ti	SEULT 12 Sequence 4, Application US/10236051 Sequence 4, Application US/10236051 Sequence 4, Application US/10236051 Sequence 4, Application US/10236051 APPLICANT: THE SCRIPPS RESEARCH INSTITUTE APPLICANT: GETURCO, Didier J. APPLICANT: ULEVITCH, Richard J. APPLICANT: TOBIAS, Peter S. APPLICANT: MATHISON, John C. TITLE OF INVENTION: METHODS AND COMPOSITIC FILE REFERENCE: SCRIP1140-4 CURRENT APPLICATION NUMBER: US 09/170,769 PRIOR PELING DATE: 1995-10-23 PRIOR APPLICATION NUMBER: US 08/373,297 PRIOR FILING DATE: 1995-01-23 PRIOR APPLICATION NUMBER: PCT/US94/05898 PRIOR FILING DATE: 1993-05-28 PRIOR APPLICATION NUMBER: US 08/373,297 PRIOR FILING DATE: 1993-05-28 PRIOR PRILING DATE: 1993-05-28 PRIOR APPLICATION NUMBER: US 08/373,297 PRIOR APPLICATION NUMBER: U	## POR INHIBITING CD14 MEDIATED CELL ACT DB 6; Length 215; 9e-66; 1
Similarity 73.8%; Pred. No. 3e-69;	US-U9-224-18UC-132 ; Sequence 132, Application US/09254180C	

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PatentIn version 3.1
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; ORGANISM: Homo sapiens
US-09-254-180C-183
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Best Local Similarity
                                                                             Best Local Similarity
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                                                          Query Match
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APPLICANT: NAKATA, MOLOMI
TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
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APPLICANT: HIGUCHI, Hirofumi
APPLICANT: NAKATA, Motomi
APPLICANT: NAKATA, Motomi
TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand of TITLE OF INVENTION: Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand FURENT APPLICATION NUMBER: US/09/254,180C
CURRENT APPLICATION NUMBER: US/09/254,180C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67.3%; Score 830.5; DB 5; Length 216; 73.1%; Pred. No. 7.3e-65; tive 18; Mismatches 35; Indels 5;
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                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/254,180C
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PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 271546/1996
                                                                                                                                                                                                                                 CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/JP97/02983
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PRIOR APPLICATION NUMBER: 231472/1996
PRIOR FILING DATE: 1996-09-02
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PRIOR APPLICATION NUMBER: 271546/1996
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PRIOR APPLICATION NUMBER: 231472/1996
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SOFTWARE: PatentIn version 3.1
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                                                                 MAEDA, Hiroaki
USHIO, Yoshitaka
                                                                                                                                                                                     FILE REFERENCE: 050006-0055
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                                              EDA, Yasuyuki
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                         APPLICANT: OKUMURA, KO
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      GENERAL INFORMATION:
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LENGTH: 216
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LENGTH: 216
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TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand FILE REFERENCE: 050006-0055 CURRENT APPLICATION NUMBER: US/09/254,180C CURRENT FILING DATE: 1999-04-15
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                                                                                                                                                               1 DVLMTQTPLSLPVSLGDQASISCKSSQSIVHSSGNTYFEWYLQKPGQSPKLLIYKVSNRF 60
                                                            5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.3%; Score 818.5; DB 5; Length 216; 72.2%; Pred. No. 8.2e-64;
tch 67.3%; Score 830.5; DB 5; Length 216; al Similarity 73.1%; Pred. No. 7.3e-65; 158; Conservative 18; Mismatches 35; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                            196 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/JP97/02983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1997-08-27
PRIOR APPLICATION NUMBER: 271546/1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 231472/1996 PRIOR FILING DATE: 1996-09-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 182, Application US/09254180C
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Search completed: June 18, 2003, 16:48:37 Job time : 28.6067 secs



Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

Sequence 1, Appli Sequence 128696, Sequence 110636, Sequence 110636, Sequence 123349, Sequence 29765, A Sequence 29765, A Sequence 74441, A Sequence 74441, A Sequence 74441, A Sequence 27722, A Sequence 27173, A Sequence 27173, A Sequence 27173, A Sequence 27173, A Sequence 27173, A Sequence 27173, A Sequence 27173, A Sequence 111, Appli

Sequence 105122, Sequence 89134, A Sequence 114644,

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APPLICANT: Frank, Dara W.
APPLICANT: Frank, Dara W.
APPLICANT: Frank, Dara W.
APPLICANT: Wiener-Kronish, Jeannine
APPLICANT: Sawa, Teiji
APPLICANT: Sawa, Teiji
APPLICANT: Fritz, Robert B.
TITLE OF INVENTION: Method of and compositions for immunization with the FILE REFERENCE: 650053.91487
CURRENT APPLICATION NUMBER: US/09/770,916
FILE REFERENCE: 650053.91487
CURRENT FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-25
PRIOR APPLICATION NUMBER: 60/109,952
PRIOR PILING DATE: 1999-13-30
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                                                                                                                                                                                                                                                                                US-09-791-537-87447
US-09-791-537-87447
US-09-791-537-93649
US-09-791-537-93651
US-09-791-537-93651
US-09-791-537-29765
US-09-791-537-2722
US-09-791-537-2722
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US-08-791-537-14884
US-08-665-8938-40
                                      US-09-791-537-138889
US-09-791-537-97993
US-09-791-537-105122
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US-09-791-537-114644
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US-09-791-537-110636
                                                                                                                                                                                                        US-09-791-537-128696
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US-09-791-537-74535
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US-09-791-537-66254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-770-916-4
; Sequence 4, Application US/09770916
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: mouse US-09-770-916-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 234
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919.5
918.5
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Sequence 58997, A
Sequence 58987, A
Sequence 127535,
Sequence 104541,
                                                                                                                                                                                       (without alignments)
1040.930 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                    1 MSVLTQVLALLLLUMLTGARC.........EATHKTSTSPIVKSFNRNEC 234
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                                                                                                                                                         June 18, 2003, 16:44:27 ; Search time 144.935 Seconds
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1: \cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

2: \cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*

3: \cgn2_6/ptodata/1/paa/US07_COMB.pep:*

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5: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

6: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

7: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

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14: \cgn2_6/ptodata/1/paa/US08_COMB.pep:*

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/ Cgn2_6/ptodata/1/paa/US091_COMB.pep:
/ Cgn2_6/ptodata/1/paa/US092_COMB.pep:
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/ Cgn2_6/ptodata/1/paa/US002_COMB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-791-537-58987
US-09-791-537-127535
US-09-791-537-104541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4569144 seqs, 644733110 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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92.9
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1165 1146 1127 1116

Result

Sequence 66254, A Sequence 73158, A Sequence 85310, A Sequence 32984, A

Sequence 40, Appl Sequence 107650,

Seguence 74535, Sequence 40,

Sequence 11, Appl Sequence 11, Appl Sequence 89445, A Sequence 14484, P Sequence 138888, Sequence 40, Appl

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                                                                                                                                                                                                                                                                               121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                                                                                              61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                        61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                                                                       GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                        1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                         0; Gaps
                                                                                                                                                                                   181 NSWIDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                               181 NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.2%; Score 1200; DB 4; Length 234; 97.0%; Pred. No. 5.7e-97;
                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SmithKline Beecham Corporation - Corporate
Patents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PPLICATION NUMBER: US/08/090,534
FILING DATE: 19930719
Best Local Similarity 100.0%; Pred. No. 5.7e-100; Matches 234; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08090534 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Sutton, Jeffrey A. REGISTRATION NUMBER: 34,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: SBC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gross, Mitchell APPLICANT: Jonak, Zdenka L. APPLICANT: Theisen, Timothy APPLICANT: Hurle, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 234 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Young, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-08-090-534-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
```

Gaps

0;

6; Indels

1; Mismatches

Matches 227; Conservative

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APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
'TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 LVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEI 126
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61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 VLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQL 66
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
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CURRENT APPLICATION NUMBER: US/09/791,537
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NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus US-09-791-537-58997
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Best Local Similarity
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LENGTH: 228
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APPLICANT: Debe, Derek
APPLICANT: Denzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
FILE REFERENCE: 261/210
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                                                                                                                                                                                                      90.4%; Score 1116; DB 21; Length 214; 98.1%; Pred. No. 1.3e-89; Live 2; Mismatches 2; Indels 0
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CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
6EQ ID NO 104541
LENGTH: 214
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
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US-09-791-537-104541
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US-09-791-537-44562
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LENGTH: 214
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APPLICANT: Deneck, Doseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
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                                                                                               7 VLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQL 66
                                                                                                                   1 MSVLTQVLALLLLMLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ
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            Query Match 92.9%; Score 1146; DB 21; Length 228; Best Local Similarity 94.3%; Pred. No. 3.1e-92; Matches 215; Conservative 4; Mismatches 9; Indels 0
                                                                                                                                                                                                                                                                                                                                                               91.3%; Score 1127; DB 21; Length 234; 91.9%; Pred. No. 1.5e-90;
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Best Local Similarity 91.95
Matches 215; Conservative
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LENGTH: 234
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APPLICANT: Debe, Derek
APPLICANT: Dalzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001_02-22
                                                                                                                                                                                                                                                                                                               APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
TITLE OF INVENTION: METHODS OF USE THEREOF
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                        121 SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 180
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0; Gaps
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                                                                                                        FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
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NUMBER OF SEQ ID NOS: 153055
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LENGTH: 213
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                                                                                                           APPLICANT: Debe, Derek
APPLICANT: Denser, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF.
FILE REFERENCE: 261/210
CORRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPRTFGGGTKLELKRADAAPTVSIFPP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 SSEQLISGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DIQMIQSPASLSASVGETVTITCRASGNIHNYLAMYQQKQGKSPQLLVYYTTLADGVPS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.5%; Score 1092; DB 21; Length 214; 96.3%; Pred. No. 1.6e-87; tive 2; Mismatches 6; Indels 0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 LIKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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                                Sequence 13851, Application US/09791537
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0
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Matches 206; Conservative
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                                                                                     APPLICANT: Bionomix, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: pdb 1CICC
S-09-791-537-13851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: pdb 1KB5L
IS-09-791-537-138889
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        S-09-791-537-13851
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LENGTH: 214
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60 QGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFG 119
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                                                                                                                                                                                                                                                                1 MSVLTQVLALL-LLWLTGARCDIQMPQSPASLSASVGETVTITCRASGNIQNYLAWYQQT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
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                                                                                                                                 Query Match 79.0%; Score 974.5; DB 21; Length 235; Best Local Similarity 80.9%; Pred No. 4.1e-77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Joliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Zivin, Robert A.
TITLE OF INVENTION: CDR-GRAFTED ANTI-TISSUE FACTOR
TITLE OF INVENTION: ANTIBODIES AND METHODS OF USE THEREOF
                                                                                                                                                                                      30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,120
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Scully, Scott, Murphy & Presser 400 Garden City Plaza
                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08480120 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 959
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TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
                                                       ; ORGANISM: synthetic construct US-09-791-537-114644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 234 amino acids
                                                                                                                                                                                   Matches 190; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-480-120-4
       LENGTH: 235
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TILLONT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
SOFTWARE: FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
                                                                                                                                 121 SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 180
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                          1 DIQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQVLVYNAKDLAEGVPS 60
21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
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                                                                                                                                                                                                                                                                                                                                         181 LTRDEYERHNSYTCEATHKTSTSPIVKSFNRNE 213
                                                                                                                                                                                                                                                                                                               201 LIKDEYERHNSYTCEATHKISTSPIVKSFNRNE 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 89134, Application US/09791537 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 114644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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LENGTH: 236
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61 WKSPKTLIYYATSLADGVPSRFSGSGSQQDYSLTISSLESDDTATYYCLQHGESPYTFGG 120
                                 61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
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APPLICANT: Bionomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
Sequence 128696, Application US/09791537 GENERAL INFORMATION:
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S-09-791-537-128696

FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFWARE: Patentin version 3.0
SEQ ID NO 128696

TYPE: PRT ORGANISM: Mus musculus S-09-791-537-128696

Query Match 78.4%; Score 967; DB 21; Length 234; Best Local Similarity 77.8%; Pred. No. 1.9e-76; Matches 182; Conservative 18; Mismatches 34; Indels 60; Gaps

1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60

61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120

121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180

181 NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234

181 NSWIDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234

earch completed: June 18, 2003, 16:56:49 ob time : 146.935 secs

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Sequence 24, Appl
Sequence 109, Appl
Sequence 30, Appl
Sequence 26, Appl
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Sequence 5, Appli
Sequence 1, Appli
Sequence 69, Appl
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Sequence 8, Appli
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Sequence 1, Appli
Sequence 100, App
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Sequence 2, Appli
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1149.899 Million cell updates/sec
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Sequence 6, Appli
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                                                                                                                                                                                                                                                                                                                            1 MSVLTQVLALLLLWLTGARC........EATHKTSTSPIVKSFNRNEC 234
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                                                                                                                                                       June 18, 2003, 16:46:17 ; Search time 22.0197 Seconds
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-153-382-19
US-09-797-941A-6
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US-09-940-166A-6
US-10-011-125-2
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US-10-194-975-109
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US-09-900-766-1
US-10-006-593-69
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US-10-216-484-11
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                                                                                                       OM protein - protein search, using sw model
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Score Match Length DB
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Sequence 2, Appli Sequence 11, Appl Sequence 10, Appl Sequence 127, Appl Sequence 127, Appl Sequence 129, Appl Sequence 129, Appl Sequence 17, Appl Sequence 17, Appl Sequence 19, Appl Sequence 24, Appl Sequence 24, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 5, Appli Sequence 5, Appli Sequence 52, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 51, Appli Sequence 118, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli Sequence 128, Appli	ILES AND VECTORS COMPLEXED THEREWITH FOR TAR 27A .0	75.0%; Score 925; DB 9; Length 238; Conservative 27; Mismatches 33; Indels 4; Gaps 1; Mismatches 33; Indels 4; Gaps 1; Mismatches 33; Indels 4; Gaps 1; MSVITQVLALLLLMLTGARCDIOMTDSPASLSASVGETVTITCRASGNIONVLAWY 56
US-09-940-166A-2 US-09-811-384-11 US-09-811-384-11 US-09-95-14-8 US-09-95-14-8 US-09-95-14-8 US-10-116-484-131 US-10-126-484-131 US-10-136-484-131 US-10-136-484-131 US-10-136-484-131 US-09-920-171-15 US-09-920-171-15 US-09-920-171-15 US-09-920-171-13 US-09-920-171-13 US-09-920-171-13 US-09-920-171-13 US-09-920-171-13 US-09-920-171-13 US-09-920-171-13 US-09-910-059-52 US-09-910-059-52 US-09-910-059-99 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2 US-09-917-410-2	GNN BCU BCU B 4	75.0%; Score imilarity 73.1%; Pred. No. 5.9e-39; Length 238 ; Conservative 27; Mismatches 33; Indels MSVITQVLALLLLMITGARCDIOMTDSPASLSASVGETVTITCRASGNI
0.5-09 0.	3, 3, 00 G	Score Pred. 27; Mis RCDIQMTQ TGDIVLTQ TGDIVLTQ I:: ESGIPARF VSIFPPSS
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214 234 234 234 238 238 218 218 218 218 218 218 218 218 218 21	ation US/0990335 16433A1 N: W, Glen R. Fryuang N: BIFUNCTIONAL N: GENE N: DELLYERY 2908-1228 ON NUMBER: US/05 ON NUMBER: US/05 I 2000-07-10 NUMBER: 09/613, I 200	75.0 cvative cvative : : : : vvLLLWVSAk : : CLLIYAAS
00000000000000000000000000000000000000	327A-4 14, Applicati 10. US20020164 INFORMATION: INT: Li, Ergu PE INVENTION: PE INVENTION: PERRENCE: 2290 APPLICATION PELING DATE: 2 OF SEQ ID NOS PER SEQ SEQ SES OF SEQ SES SES SES SES SES SES SES	Similarity 4; Conserv MSVLTQVLAL mETDTILLWV QQTQGKSPQL QQKPGQPPKL TFGGGTKLEI TFGGGTKLEI
7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ESULT 1 S-09-303-327A-4 S-09-903-327A-4 GENERAL INFORMATION: PATENT NO. US20020164333A1 GENERAL INFORMATION: APPLICANT: Nemerow, Glen R. APPLICANT: Li, Erguang TITLE OF INVENTION: BIFUNCTIONAL MY TITLE OF INVENTION: BIFUNCTIONAL MY FILE REFERENCE: 22908-1228 CURRENT APPLICATION NUMBER: US/09/CURRENT FILING DATE: 2000-07-10 PRIOR FILING DATE: 2000-07-10 NUMBER OF SEQ ID NOS: 33 SOFTWARE: FASTSEQ for Windows Vers. SOFTWARE: PRT ORGANISM: MOUSE FEATURE: NAME/KEY: PEFTIDE NAME/KEY: PEFTIDE NOGANISM: MOUSE FEATURE: NAME/KEY: PEFTIDE NOGANISM: MOUSE FEATURE: NAME/KEY: PEFTIDE NOGANISM: MOUSE FEATURE: NOGANISM: MOUSE FEA	atch scal S 174 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-795-515-5
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: PEPTIDE
                                                                     FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 TFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645Alris
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                                                181 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238
                         177 NGVLNSWIDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
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Sequence 5, Application No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Entage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           APPLICANT: Serizawa, No. US20030103976Alufusa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/216,484 CURRENT FILING DATE: 2002-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/09/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: US 09/053,583
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                          APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       Sequence 11, Application US/10216484 Publication No. US20030103976A1
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Nakahara, Kaori
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                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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120 GSGTKLEINRADIAPTVSIFPPSSEQLISGGASVVCFLNNFYFKDINVKWKIDGSERQNG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 TQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTF 118
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CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILLING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
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70.5%; Score 870; DB 9;
Best Local Similarity 73.8%; Pred. No. 6.5e-36;
Matches 169; Conservative 20; Mismatches 36
                                                                                                                                                                                                                                                       CARP-0057
APPLICATION NUMBER: US/09/795,515
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OTHER INFORMATION: Conjugate protein
                                                                                                              08/846,658
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; Publication No. US20030039655A1
; GENERAL INFORMATION:
                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,65
FILING DATE: 01-MAX-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CAF
                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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5 TQVLALLLLMLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSP 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.1%; Score 816; DB 9; Length 236; Best Local Similarity 66.2%; Pred. No. 1.3e-33; Matches 155; Conservative 28; Mismatches 51; Indels
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APPLICANT: Renshaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
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CURRENT FILING DATE: 2001-12-05
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PRIOR FILING DATE: 2000-12-05
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PRIOR FILING DATE: 2001-05-29
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Patent No. US20020001001198a1
GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
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SOFTWARE: PatentIn version 3.1
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61 GKSPQLLVYSAKTLADGVPSRFSG$GSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
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TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES TITLE OF INVENTION: SPECIFIC TO RSY F-PROTEIN AND METHODS FOR THEIR TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.5%; Score 808; DB 10; Length 234; 64.5%; Pred No. 3.1e-33; Live 29; Mismatches 54; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 65.3%; Score 806; DB 9; Length 237; Best Local Similarity 68.5%; Pred. No. 4e-33; Matches 150; Conservative 24; Mismatches 45; Indels
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TITLE OF INVENTION: Super Humanized Antibodies
FILE REFERENCE: 501231, 50121, 501231, 501231, 50121, 50121, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 5012, 50
                                                                                                                                                                FILE REFERENCE: 037003-0275759

CURRENT APPLICATION NUMBER: US/09/740,002

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: 09/335,697

PRIOR FILING DATE: 1999-06-18

PRIOR PLING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 24
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US-09-740-002-24
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Best Local Similarity
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LENGTH: 234
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                                       SEQ ID NO 26
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                                                                                      TYPE: PRT
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TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
136 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 195
                                            139 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 198
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APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Horl, No. US20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTINULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
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                                                                                               196 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                      199 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 64.7%; Score 799; DB 10;
Similarity 64.5%; Pred. No. 8.7e-33;
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CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/859,053 CURRENT FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: JP 2000-147116
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PRIOR FILING DATE: 2001-03-30
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PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
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Patent No. US20020001798A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Sequence 30, Application US/09859053 Patent No. US20020102658A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-05-16
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.6%; Score 772.5; DB 10; Length 234; 62.7%; Pred. No. 1.7e-31; tive 37; Mismatches 49; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.5%; Score 771; DB 10; Length 234; 61.1%; Pred. No. 2e-31; Live 36; Mismatches 55; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/800,729 CURRENT FILING DATE: 2001-03-08 PRIOR APPLICATION NUMBER: PCT/US00/26013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 150, Application US/09800729; Patent No. US20020068319A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.0
                                                                                                                                                                                                             Matches 146; Conservative
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Matches 143; Conservative
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-0 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                         ; ORGANISM: Homo sapiens
US-09-740-002-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 KRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQ 186
                                                                                                                                                                                                                                                                                                                                                                                                   61 GKSPQLLVYSAKTLADGVPSRFSG$GSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GTKLEIKRADAAPTVSIFPPSSEQ4TSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 VLALLLLWLTGARCDIQMTQSPAS|LSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQL 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSVLTQVLALLLLWLTGARCDIQM‡QSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
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                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 DSKDSTYSLSSTLTLSKADYEKHKWYACEVTHQGLSSPVTKSFNRGEC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             · 187 DSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                          61.7%; Score 761; DB 9; Length 245; 61.8%; Pred. No. 6.6e-31; tive 32; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%; Score 756.5; DB 10; Length 62.0%; Pred No. 1.1e-30;
tive 31; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1
CURRENT APPLICATION NUMBER: US/09/800,729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SEQ ID NO 152
                   APPLICATION NUMBER: GB 942449.8 FILING DATE: 02-DEC-1994 INFORMATION FOR SEQ ID NO: 6 SEQUENCE CHARACTERISTICS:
                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 152, Application US/09800729
Patent No. US20020068319A1
FILING DATE: 28-NOV-1995
                                                                                                                LENGTH: 245 amino acids
                                                                                                                                                                                                                                                                                                                               Matches 141; Conservative
                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                          Best Local Similarity
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182 ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reilly, Dorothea
PSPLICANT: Yangura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF FILE REFERENCE: P1793R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
FILE REFERENCE: P1867R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 61.1%; Score 754; DB 9; Length 237; Best Local Similarity 64.4%; Pred. No. 1.4e-30; Matches 141; Conservative 32; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.1%; Score 754; DB 9; Length 237; 64.4%; Pred. No. 1.4e-30;
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Matches 141; Conservative 32; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/227,694 CURRENT FILING DATE: 2002-08-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/315,209 PRIOR FILLING DATE: 2001-08-27 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : OTHER INFORMATION: anti-TF light chain JS-10-020-786-8
                 Sequence 8, Application US/10020786 Publication No. US20030073164A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10227694 Publication No. US20030077739A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetic
                                                                                                APPLICANT: Simmons, Laura C.
                                                                                                                           Klimowski, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Simmons, Laura
APPLICANT: Andersen. Dana
                                                                                                                                                                                                                                                                                                                                                                                          237
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JS-10-020-786-8
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June 18, 2003, 16:42:37 ; Search time 11.5028 Seconds (without alignments) 598.546 Million cell updates/sec I MSVLTQVLALLLLMLTGARC......EATHKTSTSPIVKSFNRNEC 234 US-09-770-916-4 Perfect score: 1234 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters: 262574 seqs, 29422922 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Listing first 45 summaries Maximum Match 100%

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*/cgn2_6/ptodata/1/iaa/pcruS_COMB.pep:*/cgn2_6/ptodata/1/iaa/pcruS_COMB.pep:*/cgn2_6/ptodata/1/iaa/packfiles1.pep:* Issued_Patents_AA:* 2.: 3.: 5.: 6.: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length DB Score Result

Sequence 5, Appli Sequence 12, Appl Sequence 12, Appl Sequence 4, Appli Sequence 3, Appli Sequence 9, Appli Sequence 8, Appli Sequence 57, Appl Sequence 34, Appl Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 2, Appli Sequence 37, Appl Sequence 5, Appli Patent No. 5189147 Sequence 5, Appli Sequence 25, Appli Sequence 8, Appli Sequence 58, Appl Sequence 23, Appl Sequence 4, Appli Patent No. 5455030 Sequence 4, Appli Sequence 61, Description Sequence 8, Sequence 4, Sequence Sequence US-08-79-8-4-3 US-08-79-8-4-3 US-08-79-824-3 US-08-79-824-12 US-08-79-824-6 US-07-690-192-2 US-08-35-400-37 US-09-423-439-58 US-09-423-439-58 US-09-11-76-8-23 US-09-11-76-8-23 US-09-11-76-8-23 US-09-11-76-8-23 US-09-11-76-8-8 PCT-US94-07659-4 US-08-303-569B-5 US-08-737-129A-4 PCT-US94-14106-61 US-07-934-373C-25 US-08-157-101A-5 US-09-170-769A-4 US-08-437-642B-25 US-08-146-206C-25 US-08-116-247-5 US-09-192-545-4 US-08-397-411-5 5455030-3 955 930.5 924 907.5 907.5 907 901 883.5 883.5 881.5 868 855.5

Length 234;

DB 5;

97.2%; Score 1200;

TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

LENGTH: 234 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein

PCT-US94-07659-4

Sequence 25, Appl

PCT-US93-07832-25

Query Match

Sequence 80, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 16, Appli Sequence 39, Appli Sequence 39, Appli Sequence 39, Appli Sequence 11, Appli Sequence 11, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli			beta -1 Mediated Inflammatory	4++					
555555555555555555555555555555555555555	ALIGNMENTS	6 5/9	and Humanized 11-1 Or Treatment of 11-1 Man	Corporation - Corp.		659	14 8		.,
232 237 237 237 237 2237 2237 2214 2214 2214 2214 2214 2214 2214 221		lication PC/TUS9407 MATION: Young, Peter Gross, Mitchell Jonak, Zdenka L. Theisen, Timothy Hurle, Mark	On, Jeffrey R. N: Recombinant N: Antibodies f N: Disorders in SEC. 21	Smithtine Beecham co Intellectual Property 9 Swedeland Road 7 of Prussia	USA 6-2799 DABLE FORM: E: Floppy disk IBM PC Compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #10	DATA: R: PCT/US94/076	8/090,5	MATION: frey A. R: 34,028	CCREI NUMBER: P50171- TION INFORMATION: (610) 270-5034
29 75.5 61.3 30 751 60.9 31 751 60.9 32 751 60.9 34 751 60.9 35 751 60.9 36 748 60.4 37 745 60.4 38 744 60.3 40 744 60.3 41 744 60.3 44 744 60.3 45 744 60.3		1 94-07659-4 ence 4, Api ERAL INFORM PPLICANT: PPLICANT: PLICANT: PLICANT:	APPLICANT: Jackson, Jarle Of Interest of Invervious Restrict OF Invervious NUMBER OF INVENTION: DINGRER OF SECURICES: 2 CORRESPONDENCE ADDRESS: 2	ADDRESSEE: Smit ADDRESSEE: Inte STREET: 709 Swe CITY: King of P.	ZIP: 19406-2799 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy: OPERATING SYSTEM: PC SOFTWARE: Patentin RC	APPLICATION DATA: FILING DATE: CLASSIFICATION.	PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0 FILLING DATE: US 0	TORNEY/AGENT INFORMATION NAME: Sutton, Jeffrey A REGISTRATION NUMBER: 34 REFERENCE/DOCKET NIMES	TELECOMMUNICATION INFORMATION:
•		RESULT PCT-US PCT-US SEQU. SEQU. GENICAL SEGU. ALICAL S		· · · · · · · ·	8		; PR]	ALT.	TEL

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CLASSIFICATION: 435
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TQVLALLLUMLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                              121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERONGVL 180
                                                                                                                        61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                            0
                                 1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; Score 1131; DB 2; Length 236; 93.9%; Pred. No. 2.1e-84;
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: U.S. Army Chemical and Biological Defense
        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                  r: Office of the Chief Counsel, Bldg E4435 Aberdeen Proving Ground
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
Pred. No. 5.3e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DAM 431-96
             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/792,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Biffoni, U. J. 39,908
REGISTRATION NUMBER: 39,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     Sequence 3, Application US/08792824 patent No. 5932449
                                                                                                                                                                                                                                                                                                   BURANS, JAMES P.
VALDES, JAMES J.
MOHYEE, ELDEFRAMI E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410-671-1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 amino acids
                                                                                                                                                                                                                                                                                         APPLICANT: EMANUEL, PETER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410-671-2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
          97.0%;
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 13 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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Matches 216; Conserv
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        west Local Similarity 97.0 fatches 227; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             21010-5423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                             ESULT 2
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THE CECEMON STRING TO SEED FOR SYNCOHEWSTPY TEGGTKL 124

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65 QLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                       125 EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT 184
67 QLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKL 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.7%; Score 1131; DB 2; Length 236; 93.9%; Pred. No. 2.1e-84; Indels (tive 2; Mismatches 12; Indels (tive
                                                                          U.S. Army Chemical and Biological Defense
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Command SIREET: Office of the Chief Counsel, Bldg E4435
                                                                                                                                                                                                                                                    DETECTION OF BOTULINUM TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/792,824
                                                                                                                                                                                                                                                                                                                                       Aberdeen Proving Ground
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: BIffont, U. J.
REGISTRATION NUMBER: 39,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: DATE: TELECOMMUNICATION:
                                                                                                                                                                                                               APPLICANT: EMANUEL, PETER A. APPLICANT: BURNS, JAMES P. APPLICANT: VALDES, JAMES J. APPLICANT: MOHYEE, ELDEFRAMI E.
                                                                                                                                                                           Sequence 9, Application US/08792824 patent No. 5932449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 410-671-1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410-671-2534
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MOHYEE, ELDEFRAWI E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 6:
APPLICANT: VALDES, JAMES J.
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 410-671-1158
410-671-2534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 233 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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U.S.A.
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21010-5423
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                                                                                                                                                                                                                                                                                                               SOFTWARE:
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                                                                                                                                                                                             COUNTRY:
                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels 0; Gaps
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                                                                                                                                                                                                                                                           ADDRESSEE: U.S. Army Chemical and Biological Defense ADDRESSEE: Command STREET: Office of the Chief Counsel, Bldg E4435 CITY: Aberdeen Proving Ground
                                                           Sequence 12, Application US/08792824
Patent No. 593249
GENERAL INFORMATION:
APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES P.
APPLICANT: WALDES, JEDEFRANI E.
TITLE OF INVENTION: DETECTION OF BOFULINUM TOXIN
NUMBER OF SOURCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DAM 431-96 TELECOMUNICATION INFORMATION: TELEPHONE: 410-671-1158 TELEFAX: 410-671-2534
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 12:
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APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
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MOLECULE TYPE: protein
US-08-792-824-12
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Best Local Similarity
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                                         US-08-792-824-12
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65 QLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.5%; Score 1080; DB 2; Length 233; 92.0%; Pred. No. 2.8e-80;
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                                                                       ADDRESSEE: U.S. Army Chemical and Biological Defense ADDRESSEE: Command
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APPLICANT: Montano, Ximena
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: METHOD FOR INACTIVATION OF PROTEIN
TITLE OF INVENTION: FUNCTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                   : Office of the Chief Counsel, Bldg E4435
Aberdeen Proving Ground
DETECTION OF BOTULINUM TOXIN
                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/792,824
                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/07690192
Patent No. 5919650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Biffoni, U. J. REGISTRATION NUMBER: 39,908
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121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GKSPQLLVYSAKTLADGVPSRFSGSGGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 NSWIDQDSKDSTYSMSSILTLIKDEYERHNSYICEATHKISISPIVKSFNRNEC 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.4%; Score 955; DB 2; Length 234; 76.9%; Pred. No. 3.7e-70; hismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/690,192
FILING DATE: 19910422
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Mismatches
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APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 37, Application US/08353400 Patent No. 5665357
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                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: BOGGEN, James M
REGISTRATION NUMBER: 32,962
REFERENCE/DOCKET NUMBER: DC1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 TELEPHONE: (609) 921-4163
TELEFAX: (609) 921-4526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 03-JUN-1994 INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
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                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 180; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein IS-07-690-192-2
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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08543-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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61 WYQQRPGQSPKLLIYWASTRTSGVPDRFTGSGSGTDFTLTISSVQAEDLAIXYCKQSY-T 119
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                                                                                                                                                                                                                                                        55 WYQQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWST 114
                                                                                                                                                                                               1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNI-----QNYLA 54
                                                                                                                                   7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: IKUO FUJII et al. TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
                                                                                         75.4%; Score 930.5; DB 1; Length 239; 75.0%; Pred. No. 3.6e-68; tive 22; Mismatches 31; Indels 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 5885816ember 15, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08737129A Patent No. 5885816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                    Best Local Similarity 75.09
Matches 180; Conservative
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                   ; MOLECULE TYPE: protein US-08-353-400-37
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                    linear
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59 TQGKSPQLLVYSAKTLADGVPSRFSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTF 118
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                                                           1 MSVLTQVLALLLL--WLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQ
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                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
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PBest Local Similarity 74.6%; Pred. No. 2.6e-66; Matches 176; Conservative 20; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/011,769A FLLING DATE: 13-Feb-1998 CLASSIFICATION: GUNROWN>
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB96/01975 FILING DATE: 13-AUG-1996
                                                                                                                                                                                                                                                                                                                          DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9612295.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 9516810.0
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                            HENNEQUIN, Laurent F.A.
                                                                                                                                                                Sequence 23, Application US/09011769A Patent No. 6436691 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: 1.44 Mb disk
                                                                                                                                                                                                                      APPLICANT: SLATER, Anthony M. BLAKEY, David C. DAVIES, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 16-AUG-1995
                                                                                                                                                                                                                                                                                                              MARSHAM, Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 235 amino acids
                                                                                                                                                                                                                                                                               John F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
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                                                                                                                             81 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVSIFPP 140
                                                                                                                                                                                                141 SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 200
                                     21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
                                                       59 TQCKSPQLLVYSAKTLADGVPSRFSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTF 118
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                   Gaps
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              25;
                                                                                                                                                                                                                                                  201 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                        Pillsbury Winthrop, L.L.P.
          15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CHEMICAL COMPOUNDS
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APPLICATION NUMBER: PCT/GB98/01294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EMERY, Stephen Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLAKEY, David Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                           Sequence 58, Application US/09423439
Patent No. 6339070
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INFORMATION FOR SEQ ID NO: 58:
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Matches 174; Conservative
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CORRESPONDENCE ADDRESS:
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75 ADGVPSRESGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPT 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 DIQMTQSPASLSASVGETVTITCRASGNI-----QNYLAWYQQTQGKSPQLLVYSAKTL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS 196
                                                                                                                                                                                            77 GVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVS 136
                               21 DIQMTQSPASLSASVGETVTITCR----ASGNIQNYLAWYQQTQGKSPQLLVYSAKTLAD 76
                                                     7; Gaps
4; Gaps
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17; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                          20; Mismatches
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03-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 34, Application US/08353400 Patent No. 5665357
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IBM PC compatible
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INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1994
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           Matches 169; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC (
OPERATING SYSTEM:
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                                                                                                                                                         APPLICANT: LETURCQ, Didier
APPLICANT: MORIATRY, Ann
APPLICANT: ULEVITCH, Richard
APPLICANT: TOBIAS, Peter
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 GSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVSIFPPSSE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GSGSGTDYSLTISNLEGEDFATYFCQRGDTLPWTFGGGTKLEIKTADAAPTVSIFPPSSE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTK 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 QLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 MTOSPASLSASVGETVTITCRASGNIQNYLAWYQOTOGKSPQILVYSAKTLADGVPSRFS 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Process for Generating Specific Antibodies NOWBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73.0%; Score 901; DB 5; Length 218; 77.5%; Pred. No. 7.9e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 73.5%; Score 907; DB 4; Length 211; Best Local Similarity 81.0%; Pred. No. 2.5e-66; Matches 171; Conservative 18; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 DEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 DEYERHNSYTCEATHKTSTSPIVKSFNRNEC 211
                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/170,769A CURRENT FILING DATE: 1998-10-13 PRIOR APPLICATION NUMBER: US/08/070,160 PRIOR FILING DATE: 1993-05-28
                                                                                                                                                     APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/14106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57, Application PC/TUS9414106
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              Sequence 8, Application US/09170769A Patent No. 6444206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 218 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                          PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-14106-57
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                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Murine
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                                                                                     3-09-170-769A-8
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INFORMATION: (215) 568-3100
TELERAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TUBNGTH: 235 amin
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                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear; MOLECULE TYPE: protein US-08-116-247-5
                                                                                                  ZIP: 19103
COMPUTER READABLE FORM:
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                                     Philadelphia
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 GGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 KSGTSPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEAEDAATYYCQQWSSNPFTF 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 VLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKISTSPIVKSFNRNEC 235
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                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.6%; Score 883.5; DB 2; Length 235; Best Local Similarity 72.0%; Pred. No. 2.3e-64; Matches 170; Conservative 21; Mismatches 42; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jolliffe, Linda K.
APPLICANT: Zivin, Robert A.
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: CD3 Specific Recombinant Antibody
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                            APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
APPLICANT: Enteage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 31
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
             Sequence 5, Application US/08303569B
Patent No. 5859205
GENERAL INFORMATION:
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Patent No. 5929212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 amino acids
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APPLICATION NUMBER: US
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                   USA
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US-08-303-569B-5
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Humanised anti-Fas Humanised anti-Fas T84.12 119th Chain T84.12 L4-12-1 119 FAB Light Chain fo Murine A5B57 Light Plasmid pEE14/A5B7

Murine anti-Fas an

FAB light chain fo Kappa anti-carcino

antibody FB3 MH1 monoclonal ant Anti-bGH monoclona

Mouse anti-bovine Mouse antibody FB3

Mouse antibody F4-

MAD 55.1 light cha Mouse agglutinatio Anti-tobacco mosai Chimeric antibody

L chain subunit of Anti-human Fas mon Monoclonal antibod

Anti-human Fas ant Mouse immunoglobul V11ys-HuCkappa reg Mouse 6D9 catalyti rype II collagen f

WOW-1 Fab light ch TRA-8 light chain. Monoclonal antibod

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Murine anti-BGH MA Recombinant 4G10 a

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Interleukin-1 beta; IL-1 beta; recombinant antibody; humanised antibody; chimeric antibody; antibody engineering; monoclonal antibody; MAb; SK48-E26; inflammation; therapy.
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                                                                                                                                                   AAR75457
AAR75459
AAW01751
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AAR53802
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AAR43674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Sig_peptide
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ABB76
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/label= FR1
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Homo sapiens.
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Mouse monoclonal a
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                                                                                        (without alignments) '968.107 Million cell updates/sec
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Antibody 3G2
                                                                                                                                             1 MSVLTQVLALLLLHWLTGARC.......EATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                /SIDSZ/gcgdata/geneseqy-embl/AA1983.DAT:*
/SIDSZ/gcgdata/geneseqy-embl/AA1984.DAT:*
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/SIDSZ/gcgdata/geneseqy/geneseqp-embl/AA1989.DAT:*
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                                                                        June 18, 2003, 16:41:53 ; Search time 32.2079 Seconds
                                                                                                                                                                                                                                                                                                                                                /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*/SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                       908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                   OM protein - protein search, using sw model
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Listing first 45 summaries
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AAR76087
AAE18371
AAW15935
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AAY30118
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Database

Sequence:

Run on:

Searched:

1131 1131 1131 1080 955 947 930.5

Result Ş.

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GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSVLTQVLALLLLALLTGARCDIQMTQSPASLSASVGETVTITCRASGNIHNYLTWYQQKQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequences of the heavy chain (AAW11917) and light chain (AAW11918) of anti-human interleukin-1 beta (IL-1 beta) murtine monocional antibody (MAD) St48-E26 were deduced form nucleic acids (AAT51436-37) derived from hybridoma St48-E26. The heavy and light chains, esp. the complementarity determining region sequences, can be utilised in novel recombinant chimeric and humanised antibodies (see also AAW11919-20) useful for the treatment and prevention of IL-1 mediated inflammatory disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1200; DB 16; Length 234; Pred. No. 9.4e-69;
                                                                                /note= "complementarity determining region 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant and humanised chimeric antibodies against human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                             Jonak ZL, Theisen TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for preventing and treating
                                                                                                 (Claim 10, page 48)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin-mediated inflammatory disorders
                                                                                                                                /label= FR4
/note= "framework region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                  /note= "framework region 3"
                                                                                                                                                                                  /label - Constant_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 38-39; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                             Hurle MR, Jackson JR,
                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
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97.0%;
                                                                 /label= CDR3
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                  /label= FR3
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.108
                                                                                                                                                                ..234
                                                   .117
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1995-066868/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT51437.
                                                                                                                                                                                                                                                                                 07-JUL-1994;
                                                                                                                                                                                                                                                                                                               09-JUL-1993;
                                                                                                                                                                                                                                                                                                                                 04-MAR-1994;
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                                                                                                                                                                                                                                                19-JAN-1995
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This sequence represents the light chain of BotFab 5,

a murine recombinant antibody fragment (rFab) specific to

a murine recombinant antibody fragment (rFab) specific to

botulinum toxin types A and B. A cDNA library was made from mouse mRNA

solated from mice immunised with human pentavalent toxoid. The cloned

mouse heavy and light chains were expressed in phage display libraries

and screened for their ability to bind to botulinum toxin types A or B.

The clones were then isolated and sequenced. Botulinum neurotoxin is

produced as several antigenically distinct serotypes (A-G) and is

non-covalently associated with non-neurotoxic proteins. The rFab of

this invention binds to the non-neurotoxic proteins that are found in

neurotoxin complexes A and B. Such antibody fragments are able to

act as immunosensors for detecting botulinum toxins in food and

are less expensive to produce than monoclonal antibodies as they can be

isolated from large scale bacterial cultures. Also, the affinity of an

ireth may be altered by mutagenesis of its gene and subsequent screening
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                           Murine anti-botulinum toxin antibody fragment (BotFab 5) light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                            Recombinant antibody fragment; rFab; botulinum; neurotoxin;
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                                                                                                                                                                                                                                                                                                                                                       'Valdes JJ;
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93.9%; Pred. No. 2.2e-64;
tive 2; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                         Burans JP, Eldefrawi ME, Emanuel PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Columns 17-20; 24pp; English.
                                                                                               Clostridium botulinum; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of botulinum toxin
                                                                                                                                                                                                                                      97US-0792824.
                                                                                                                                                                                                                                                                                        97US-0792824.
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             20-0CT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                        (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the expressed rFabs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAX86664
                                                                                                                                  Mus musculus.
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RESULT 3

AAY30116 standard; Protein; 236 AA.

RESULT 2

AAY30116;

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AAY30120 standard; Protein; 236 AA

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AAX30122 standard; Protein; 236 AA
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a murine recombinant antibody fragment (Frab) specific to
botulinum toxin types A and B. A cDNA library was made from mouse mRNA
isolated from mice immunised with human pentavalent toxoid. The cloned
mouse heavy and light chains were expressed in phage display libraries
and screened for their ability to bind to botulinum toxin types A or B.
The clones were then isolated and sequenced. Botulinum neurotoxin is
produced as several antigenically distinct scrotypes (A-G) and is
non-covalently associated with non-neurotoxic proteins. The Frab of
this invention binds to the non-neurotoxic proteins that are found in
neurotoxin complexes A and B. Such antibody fragments are able to
act as immunosensors for detecting botulinum toxins in food and
are less expensive to produce than monoclonal antibodies as they can be
isolated from large scale bacterial cultures. Also, the affinity of an
in any be altered by mutagenesis of its gene and subsequent screening
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                                                                                       Murine anti-botulinum toxin antibody fragment (BotFab 20) light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                            Recombinant antibody fragment; rFab; botulinum; neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the light chain of BotFab 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Columns 31-34; 24pp; English.
                                                                                                                                           Clostridium botulinum; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of botulinum toxin
                                                                                                                                                                                                                                                                                                97US-0792824.
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                                               20-OCT-1999 (first entry)
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65 QLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKL 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the light chain of BotFab 22, a murine recombinant antibody fragment (Frab) specific to botulinum toxin types A and B. A GNA library was made from mouse mRNA isolated from mice Immunised with human pertavalent toxoid. The cloned mouse heavy and light chains were expressed in phage display libraries and screened for their ability to bind to botulinum toxin types A or B. The clones were then isolated and sequenced. Botulinum neurotoxin is
                                                                           Murine anti-botulinum toxin antibody fragment (BotFab 22) light chain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.7%; Score 1131; DB 20; Length 236; 93.9%; Pred No. 2.2e-64; ive 2; Mismatches 12; Indels 0;
                                                                                                                                                       Recombinant antibody fragment; rFab; botulinum; neurotoxin; Clostridium botulinum; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burans JP, Eldefrawi ME, Emanuel PA, Valdes JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Columns 39-40; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0792824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0792824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0011013.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.74
Best Local Similarity 93.95
Matches 216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the expressed rFabs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-492692/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX86667
                                                                                                                                                                                                                                                                              Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-1997;
20-0CT-1999
                                                                                                                                                                                                                                                                                                                                                  US5932449-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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RESULT 5 4AY30118

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recombinant, intracellularly expressed anti-protein antibodies (or fragments). The protein function to be inhibited is preferably p21(ras). It is especially inhibited by the monoclonal antibody Y13.259. This sequence represents the light chain of the Y13.259 antibody. The method may be used to inhibit the activity of specific proteins in cells and eliminate undesirable biological responses, e.g. it may be used to treat conditions associated with the over-expression or overactivity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GKSPQLLIYYASSLQDGVPSRFSGSGSGTQFSLKISNMQPEDEGVYYCQQAYKYPSTFGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GTKLELKRADAAPTVSIFPPSMEQLTSGGATVVCFVNNFYPRDISVKWKIDGSEQRDGVL 180
  127 EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAIPTQLLGLLLLWITDAICDIQMTQSPHSLSASLGETVSIECLASEGISNYLAWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for inhibiting protein function using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           target protein. In this way the method may be used to treat cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibition; function; recombinant; p21; ras; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting protein function using recombinant, intracellularly
                                                          185 DODSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKS 228
                                                                                       187 DODSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPLSRA 230
                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-p21(ras) monoclonal antibody Y13-259 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neoplasms, by targeting proteins encoded by oncogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        light chain; activity; cancer; neoplasm; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.4%; Score 955; DB 20; 76.9%; Pred. No. 3e-53; tive 25; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Column 15-16; 23pp; English.
                                                                                                                                                                                                                                                    AAY14557 standard; Protein; 234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0690192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91US-0690192.
                                                                                                                                                                                                                                                                                                                                                              31-AUG-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Montano X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-394621/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX79347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5919650-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barbacid M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180;
                                                                                                                                                                                                                                                                                                               AAY14557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                    RESULT 6
                                                                                                                                                                                                                             AAY14557
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                                                          ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 QLLVYNAKTLADGVPSRFSGSGSTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 EIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 TQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSP 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 TAAAGLLLLAAQPAMADIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are also useful in health care and in military applications. They are less expensive to produce than monoclonal antibodies as they can be isolated from large scale bacterial cultures. Also, the affinity of an rFab may be altered by mutagenesis of its gene and subsequent screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse heavy and light chains were expressed in phage display libraries and screened for their ability to bind to botulinum toxin types A or B. The clones were then isolated and sequenced. Botulinum.neurotoxin is produced as several antigenically distinct serotypes (A-G) and is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the light chain of BotFab 1, a murine recombinant antibody fragment (rFab) specific to botulinum toxin types A and B. A cDNA library was made from mouse mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated from mice immunised with human pentavalent toxoid. The cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-covalently associated with non-neurotoxic proteins. The reab of this invention binds to the non-neurotoxic proteins that are found in neurotoxin complexes A and B. Such antibody fragments are able to act as immunosensors for detecting botulinum toxins in food and
                                                                                                                                                                                                                                                                                                                                     Murine anti-botulinum toxin antibody fragment (BotFab 1) light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 DQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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Recombinant antibody fragment; rFab; botulinum; neurotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eldefrawi ME, Emanuel PA, Valdes JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Columns 25-26; 24pp; English.
                                                                                                                                                                  AAY30118 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium botulinum; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detection of botulinum toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0792824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0792824.
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                                                                                                                                                                                                                                                                             20-OCT-1999 (first entry)
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Matches 206; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSA ) US SEC OF ARMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the expressed rFabs.
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WPI; 1999-492692/41.

Burans JP,

30-JAN-1997; 01-FEB-1996; 30-JAN-1997;

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X X O X & X

US5932449-A. 03-AUG-1999

282

N-PSDB; AAX86665.

0; Gaps

Indels

233 AA;

Sequence Query Match

DB 20; Length 234;

Mus musculus

Region Region Region Region

AAW27089;

AAW27089 RESULT 7

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JP09154587-A.

09-MAY-1996; 02-NOV-1995;

Sequence

Query Match

Matches

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17-JUN-1997.

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55 WYQQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWST 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNI-----QNYLA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036) chains of 55.1 were isolated, and F(ab)', F(ab)2, Fab, Fv, scFv or V-min humanized 55.1 constructs have been expressed in myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAb 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
                                                                                                                                                                                                                                                                                                       Antigen binding structure; complementarity determining région; CDR; CA55.1; colorectal cancer; tumor-associated antigen; hybridoma; monoclonal antibody; MAb; immunotherapy; therapy; diagnosis; transgenic animal; transgenic plant; antibody engineering;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen binding structures containing CDRs recognising the CA55.1 antigen - produced by hybridomas and host cells, for use in the diagnosis and therapy of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ## Match 75.4%; Score 930.5; DB 16; Length 239; Local Similarity 75.0%; Pred. No. 1.1e-51; nes 180; Conservative 22; Mismatches 31; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copley CG, Hall SM, Paterson DS;
                       201 LIKDEYERHNSYICEATHKISTSPIVKSFNRNEC 234
                                          /label= Mat_protein
/note= "claim 3, page 98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig.16; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                    humanized antibody; immunotoxin.
                                                                                                                                                     AAR76087 standard; Protein; 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94GB-0011089.
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                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21..239
                                                                                                                                                                                                                                                                      MAb 55.1 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Boot C, Wright AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1995-215262/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells and E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ94036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-1994;
                                                                                                                                                                                                                              21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9515382-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blakey DC,
                                                                                                                                                                                            AAR76087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rose MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                     RESULT 8
                                                                                                                                        AAR76087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVSIFPP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the mouse monoclonal antibody B9 light chain (B9L), which binds specifically to human blood apolipoprotein B-100. The nucleic acid can be used in a method for the preparation of a reconstituted antibody which specifically binds human plasma apolipoprotein B-100. The antibody can be used as a reagent for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
181 DSVTDQDSKDSTYSMSSTLSLTKVEYERHNLYTCEVVHKTSSSPVVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining the concentration of human plasma apolipoprotein B-100 in a sample. The antibody is also useful in a drug composition for selectively removing arteriosclerotic lipoproteins containing human
                                                                                                                                                                                                                                             Human plasma apolipoprotein B-100; arteriosclerotic lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding mouse antibody binding human plasma apo-lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.7%; Score 947; DB 18; Length 214; 83.6%; Pred. No. 8.9e-53; tive 13; Mismatches 22; Indels (

    useful for removing arteriosclerotic lipoprotein(s)

                                                                                                                                                                                                         Mouse monoclonal antibody B9 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KOAD ) KOREAN SCI & TECHNOLOGY RES CENT.
                                                                                                                                                                                                                                                                                                                                           Socation/Qualifiers
                                                                                          AAW27089 standard; Protein; 214 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 6; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108..214
/label= Ckappa
                                                                                                                                                                                                                                                                                                                                                                                                                                      89..97
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                    /label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plasma apolipoprotein B-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96JP-0114492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95KR-0039459
                                                                                                                                                                   18-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-367067/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
hes 179; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT85091.
                                                                                                                                                                                                                                                                  antibody; Fab.
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ESULT 9 AE1837

1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNI----QNYLAWY 56

permit targetting of viral and bacterial vectors to cells that express targetted receptors. Diseases that can be targetted include cancers, vascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence is human penton base monoclonal antibody, DAV-1

light chain.

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117 TFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176
                                                                                          57 QQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPY 116
177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW15935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW15935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer; vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder; hyperproliferative disorder; hormonal disorder; DAV-1 light chain;
                                                                                                                                                              120 LRTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE 179
      115 PYTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSE 174
                                                                                                                                 175 RONGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention relates to a bifunctional molecule comprising an
                                   Human penton base monoclonal antibody, DAV-1 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; vasotropic; ophthalmological.
                                                                                                                                                                                                                                                                                                                                                            AAE18371 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 93; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUL-2001; 2001WO-EP07878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-2000; 2000US-0613017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cells lacking av integrins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-171707/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS AG
(NOVS ) NOVARTIS-ERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nemerow GR, Li E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD29309.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200204522-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2002.
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The present sequence represents the variable region of the light chain of antibody 3G2, produced by the hybridoma ZAA3G2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid esters enantioselectively. Preferably the esters are 4-nitro-
benzyl esters and the esterified amino acids are amino-protected.
Also disclosed are new hybridomas expressing the catalytic antibodies,
especially ZAA7G12 (FERM BP-4947) and ZAA3G2 (FERM BP-4946). The
antibodies are raised in mice using the compound p-nitrobenzyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           They are used for efficient resolution of racemic amino acids with high optical selectivity, giving optically active amino acids useful for the production of optically active drugs and chiral separation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The patent discloses new catalytic antibodies which hydrolyse amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4-carboxy-1-(benzyloxycarbonylamino)-butyl]phosphonate as hapten.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catalytic antibody for enantioselective hydrolysis of amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.9%; Score 924; DB 17; Length 216;
                                                                                                                                                                                                                     catalytic antibody; enantioselective hydrolysis; hybridoma; ZAA7G12; ZAA3G2; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - also new hybridoma secreting the antibody
                                                                                                                                                                                        Antibody 3G2 light chain variable region.
                                                                                                                                                                                                                                                                                                                                      /note= "encoded by TAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 39; 49pp; Japanese.
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                            AAW15935 standard; Protein; 216 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinoshita K, Tanaka F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PROT-) PROTEIN ENG RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                               95WO-JP00462.
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                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                     Misc-difference 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT87818.
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                                                                                                                                                                                                                                                                                                                                                                    WO9629426-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-1995;
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(SANY ) SANKYO CO LID.
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              0
                                                                                 81 RFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPYTFGGGTKLEIKRADAAPTVSIFPP 140
                                                                                              61 RFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGGGTKLEIKRADAAPTVSIFFP 120
                                                                                                                                SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 200
                                                                                                                                                      121 SSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT 180
                                              21 DIQMTQSPASLSASVGETVTITCRASGNIQNYLAWYQQTQGKSPQLLVYSAKTLADGVPS 80
             0; Gaps
                                                                                                                                           thrombopenia purpura; insulin-dependent diabetes; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS; transplant rejection; therapy; complementarity determing region;
                                                                                                                                                                                                                                                                                                                                                         HFE7A, monoclonal antibody; mouse; Fas; humanised antibody; apoptosis; HFE7A; autoimmune disease; Hashimoto's disease; systemic lupus erythematosus; graft versus host disease; Sjogren syndrome; perniclous anaemia; Addison's disease; scleroderma; Goodpasture syndrome; Crohn's disease; rheumatoid arthritis; autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis; Basedow's disease;
81.3%; Pred. No. 2.6e-51; ative 15; Mismatches 25; Indels
                                                                                                                                                                             201 LIKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                         181 LTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label = Mat_protein
                                                                                                                                                                                                                                                            AAW83042 standard; Protein; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label= Variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label = Constant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "claim 9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "claim 9"
                                                                                                                                                                                                                                                                                                                                   Anti-Fas MAb HFE7A light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14..58
/label= CDR_L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= CDR_L2
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97JP-0169088.
                                                                                                                                                                                                                                                                                                           15-MAR-1999 (first entry)
          Matches 174; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113..121
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1997;
25-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1997;
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                                                                                                                                                                                                                                                                                     AAW83042;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                        RESULT 11
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57 QQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 NGVLNSWIDQDSKDSTYSMSSTLTLITKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      murine; complementarity determining region; CDR; human Fas; Fas ligand; apoptosis modulator; programmed cell death; autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNI----ONYLAWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells. They are used to evaluate, in animal models, treatments of diseases that involve Fas/Fas ligand interactions, and also to treat such diseases, including autoimmune disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft versus host disease, Sjogren syndrome, pernicious anaemia, Addison's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis, AIDS and transplant rejection (all claimed).
                                                                                                                                                                                                                               New antibodies and proteins bind conserved epitope of Fas antigen used to evaluate drugs in animal models and to treat Fas-associated diseases e.g. autoimmune disease, allergy, atopy, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the amino acid of the light chain of murine anti-human Fas monoclonal antibody HFE7A. cDNA (see AAV70130) encoding the light chain was obtained from HFE7A-secreting hybridoma (FERM BP-5828) RNA by RT-PCR (see AAV70127-28). The invention provides humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA by RT-PCR (see AAV820127-28). The invention provides humanised HFE7A antibodies (see AAV83031-37) produced by CDR grafting. There antibodies are capable of inducing apoptosis in abnormal cells expressing Fas, and of inhibiting Fas-induced apoptosis in normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 74.4%; Score 918; DB 19; Length 238; Best Local Similarity 72.3%; Pred, No. 6.7e-51; Matches 172; Conservative 28; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828;
           Jun O, Kimihisa I;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Reference Example 4; Page 189-190; 292pp; English.
                                           Tohru T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse anti-Fas antibody HFE7A light chain.
eyuki H, Hiroko Y, J
Nobufusa S, Shin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB14748 standard; Protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                    myocarditis, hepatitis and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
   Hideyuki H,
                                                                                                                 WPI; 1998-543440/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 AA;
                                                                                                                                                                N-PSDB; AAV70130.
                                       Masahiko O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 - NOV - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB14748;
       Akio S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB14748
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hepatitis; AIDS; graft rejection; light chain.

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TFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 QQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (complementarity determining regions) to antibody HFETA. Wa its interaction with Fas, the antibody of the invention acts as a modulator of apoptosis. The compositions of the invention may therefore be used in the treatment or prevention of conditions such as autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergy, atopy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft rejection. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSVLTQVLALLLLMLTGARCDIQMTQSPASLSASVGETVTITCRASGNI----QNYLAWY 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 METDTILLWWMMLWIPGSTGDIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 NGVLNSWIDQDSKDSTYSMSSTLTLTKDEYERHNSYICEAIHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or diseases caused by an abnormality in the Fas/Fas ligand system containing an anti-Fas antibody as the active component. The anti-Fas antibody is either the murine anti-human Fas monoclonal antibody HFE7A, or a humanised version of HFE7A containing identical CDRs
                                                                                                                                                                                                                                                                                                                                                                         Preventive or treating agent for the diseases caused by an abnormality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to compositions for the prevention or treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic; anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      light chain of the murine anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma HFE7A (FERM-BP-5828)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the Fas/Fas ligand system e.g. autoimmune diseases, contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 74.4%; Score 918; DB 21; Length 238; Best Local Similarity 72.3%; Pred. No. 6.7e-51; Matches 172; Conservative 28; Mismatches 34; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - :: :- - :: = = <del>- : : :</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 70; 139pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW90898 standard; Protein; 238 AA.
                                                                                                                                              99JP-0278301.
                                                                                                                                                                                            98JP-0276883.
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                                                                                                                                                                                                                                               (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                WPI; 2000-485645/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            anti-Fas antibody
                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA72109.
                                           JP2000169393-A.
Mus musculus.
                                                                                                                                                                                            30-SEP-1998;
                                                                                                                                            30-SEP-1999;
                                                                                           20-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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This invention describes a novel humanized anti-Fas antibody-like
molecule (1) that, induces apoptosis in cells with an abnormal Fas/Fas
ligand system, by landing to Fas on the cell surface, and prevents
capoptosis in cells with a normal system, by inhibiting binding between
Fas and its ligand. The products of the invention have anti-inflammatory,
anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral,
immunomodulatory, dermatological, immunosupressive, thyromimetic,
antirheumatic, nephrotropic, antihinfertility, neuroprotective,
antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
antiarteriosclerotic, randiant and hepatropic activity. (I) induce
capoptosis by binding to cell surface Fas or inhibit it by competitive
inhibition of ligand binding. (I) are used to treat and/or prevent
diseases associated with the Fas/Fas ligand system, especially systemic
lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
anemia, Addison's disease, scleroderma, Goodpasture syndrome, crohn's
disease, autoimmune hemolytic anemia, sterility, mysatheria gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (B, C or D) or alcoholic), and transplant rejection. (I) selectively inhibit apoptosis in normal cells but selectively induce it in abnormal cells. They bind to both human and murine Fas, so can be evaluated in murine disease models. (I) act on the active site of Fas, i.e. they mimic the native ligand, do not induce liver disease, and have reduced risk of inducing a human anti-murine antibody response. This sequence represents a murine anti-Fas monoclonal antibody HFE7A light chain described in the
dermatological; immunosuppressive; thyromimetic; anti-Fas; nephrotropic; antilnfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSVLTQVLALLLLWLTGARCDIQMTQSPASLSASVGETVTITCRASGNI----QNYLAWY 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 METDTILLMVMMLWIPGSTGDIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized anti-Fas antibody, useful for treating or preventing e.inflammatory or autoimmune disease, induces apoptosis selectively in cells with abnormal Fas-Fas ligand systems
                                                                                                                                                                             insulîn dependent diabetes mellitus; arterioscierosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.4%; Score 918; DB 21; Length 238; 72.3%; Pred. No. 6.7e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example reference 4; Page 104; 263pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.3%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                          99EP-0307711.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAA11547
                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1998;
                                                                                                                                                                                                                                                                                                            EP990663-A2
                                                                                                                                                                                                                                                                                                                                                             05-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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57 QQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPY 116

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121 TFGGGTKLEIKRADAAPTVSIFPP$SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 180
                                        177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SANY ) SANKYO CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP2001342149-A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                          30-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                      ABB74913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                         RESULT 15
                                                                                                                                                           ABB74913
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                                                                                                                                                                                                                      XX
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117 TFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176
                                                        117 TFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGAŞVVCFLNNFYPKDINVKWKIDGSERQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 QQTQGKSPQLLVYSARTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPY 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in a cell expressing Fas. The agent has immunosuppressive and antiallerigic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a peptide, useful to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a preventive or treating agent for diseases caused by abnormality in Fas/Fas ligand system containing as the active component an antibody having as the light chain subunit a polypeptide containing residues 1.218 of one of 3, 239 residue amino acid sequences, or residues 1-451 of one of 3, 470 residue amino acid sequences, fully defined in the specification and having an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSVLTQVLALLLLMLTGARCDIQMTQSPASLSASVGETVTITCRASGNI----QNYLAWY 56
                                                                                                                                                         181 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238
                                                                                                                                     177 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drug containing humanised anti-Fas antibody, used for preventing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          light chain subunit; apoptosis; immunosuppressive; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.4%; Score 918; DB 23; Length 238; 72.3%; Pred. No. 6.7e-51; tive 28; Mismatches 34; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
                                                                                                                                                                                                                                                                                                                                                                                                  Humanised anti-Fas antibody related peptide SEQ ID NO 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating autoimmune diseases, allergy, and atopy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6 (Preparatory); Page 26; 194pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disease; allergy; atopic.
                                                                                                                                                                                                                                                                            ABB74867 standard; Peptide; 238 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2000; 2000JP-0090918.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-MAR-2001; 2001JP-0093106
                                                                                                                                                                                                                                                                                                                                                       26-APR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 72.3%
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-145113/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2001342148-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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57 QQTQGKSPQLLVYSAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 TFGGGTKLEIKRADAAPTVSIFPP$SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a preventive or treating agent for diseases caused by abnormality in the Fas/Fas ligand system containing, as the active component, an antibody having a light chain subunit and a heavy chain subunit and an activity of combining specifically with mammalian Fas and an activity of inducing apoptosis in a cell expressing Fas. The agent has antialiargic, immunosuppressive and apoptotic activity and is used for preventing and treating autoimmune diseases, allergy, atopy and others. The present sequence is that of a peptide useful to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
181 NGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 NGVLNSWTDQDSKDSTYSMSSTLTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 METDTILLWVMMLWIPGSTGDIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSVLTQVLALLLLWLTGARCDIQM†QSPASLSASVGETVTITCRASGNI----QNYLAWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; Fas/Fas ligand systém; Fas; antibody; light chain;
heavy chain; apoptosis; antiallergic; immunosuppressive; apoptotic;
autoimmune disease; allergy; atopy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drug for preventing or treating e \beta , autoimmune disease or allergy, comprises humanised anti-Fas antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.4%; Score 918; DB 23; Length 238; 72.3%; Pred No. 6.7e-51; Live 28; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised anti-Fas antibody related peptide SEQ ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 65; 154pp; Japanese.
                                                                                                                                                                                                                                                   ABB74913 standard; Peptide; 238
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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Matches 172; Conservative
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Search completed: June 18, 2003, 16:44:19 Job time : 33.2079 secs